BLAST Basic Local Alignment Search Tool

-

Edit and Resubmit Save Search Strategies Formatting options Download

Nucleotide Sequence (11111 letters)

Results for: lcl|24839 None(11111bp) ▾

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID
    lcl|24839
Description
    None
Molecule type
    nucleic acid
Query Length
    11111   SEQ ID NO: 13

Database Name
    nr
Description
    All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS,environmental samples or phase 0, 1 or 2 HTGS sequences)
Program
    BLASTN 2.2.19+ Citation

Reference
Zheng Zhang, Scott Schwartz, Lukas Wagner, and Webb Miller (2000), "A greedy algorithm for aligning DNA sequences", J Comput Biol 2000; 7(1-2):203-14.
Other reports: Search Summary [Taxonomy reports] [Distance tree of results]

Search Parameters

Program	blastn
Query range	397-1772
Word size	28
Expect value	10
Hitlist size	100
Match/Mismatch scores	1,-2
Gapcosts	0,0
Low Complexity Filter	Yes
Filter string	L;m;
Genetic Code	1

Database

Posted date	Nov 16, 2008 5:48 PM
Number of letters	259,029,644
Number of sequences	7,734,480
Entrez query	none

Karlin-Altschul statistics

Params	Ungapped	Gapped

Lambda	1.33271	1.28
K	0.620991	0.46
H	1.12409	0.85

Results Statistics

| Length adjustment	33
Effective length of query	1343
Effective length of database	25143791804
Effective search space	33768112392772
Effective search space used	33768112392772

Graphic Summary

Distribution of 112 Blast Hits on the Query Sequence

?]

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.
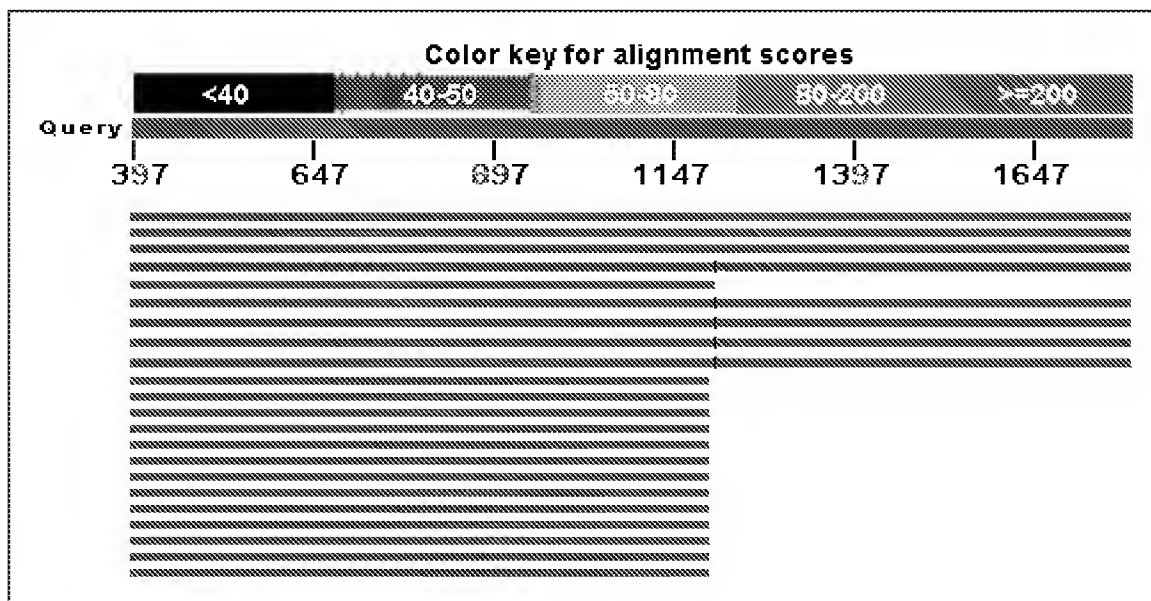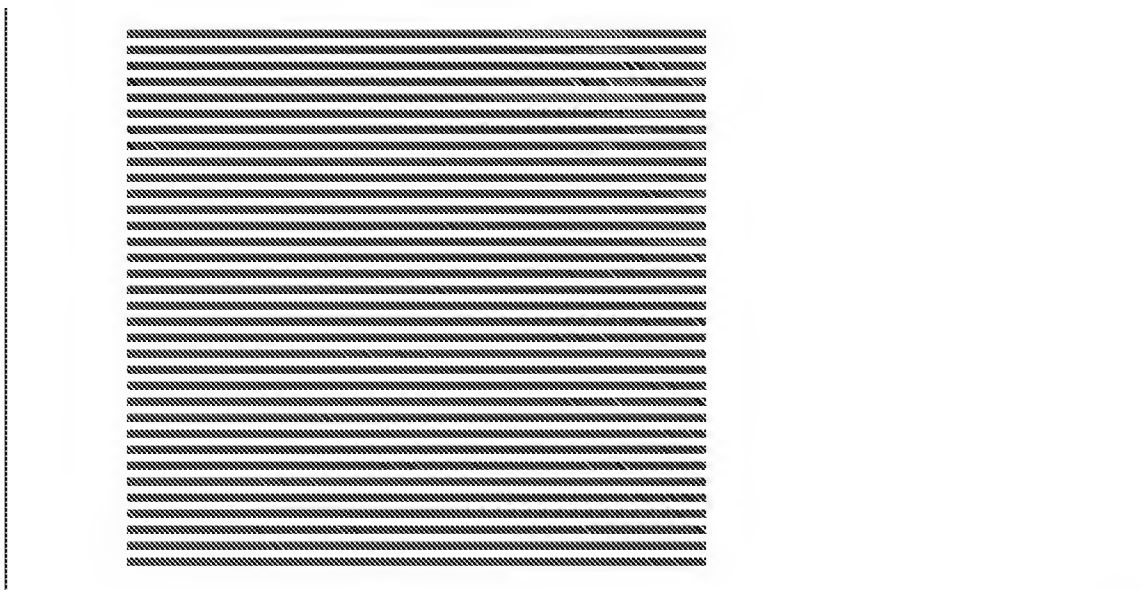
Descriptions

Legend for links to other resources: ▨ UniGene ▤ GEO ⬛ Gene ▨ Structure ▨ Map Viewer

```
Sequences producing significant alignments:
(Click headers to sort columns)
```

Accession	Description					
AB237837.1	Hepatitis C virus full-length replicon pFGR-JFH1 RNA, complete sequence	2542	2542	100%	0.0	100%
AB114136.1	Hepatitis C virus replicon pSGR-JFH1 gene for neomysin resistance gene product, hepatitis C virus nonstructural protein, complete cds	2542	2542	100%	0.0	100%
AF311318.1	Retroviral vector NIT, complete sequence	2390	2390	99%	0.0	97%
AB119282.1	Hepatitis C virus gene for Fusion protein, Feo, complete cds	1483	2532	100%	0.0	100%
DQ320121.1	Binary vector pBINPLUS/ARS, complete sequence	1483	1483	58%	0.0	100%
AJ242651.1	Hepatitis C virus replicon I377/NS2-3'UTR	1483	2532	100%	0.0	100%
AJ242654.1	Hepatitis C virus replicon I389/NS3-3'UTR	1483	2532	100%	0.0	100%
AJ242653.1	Hepatitis C virus replicon I389/NS2-3'UTR	1483	2532	100%	0.0	100%
AJ242652.1	Hepatitis C virus replicon I377/NS3-3'UTR	1483	2532	100%	0.0	100%
FJ155667.1	Allelic replacement vector pJC84, complete sequence	1471	1471	57%	0.0	100%
AB434475.1	Synthetic construct gfpuv5, aphA genes for green fluorescent protein UV5, kanamycin resistance, complete cds, clone: pT2	1471	1471	57%	0.0	100%
AB434474.1	Synthetic construct gfpuv5, aphA genes for green fluorescent protein UV5, kanamycin resistance, complete cds, clone: pT1	1471	1471	57%	0.0	100%
AB434472.1	Synthetic construct aphA, pyrE, gfpuv5 genes for kanamycin resistance, orotate phosphoribosyltransferase, green fluorescent protein UV5, complete cds, clone: OSU12-pyrE	1471	1471	57%	0.0	100%
AB293446.1	Saccharomyces cerevisiae gene for aquaporin Aqy1, complete cds, clone: COS5	1471	1471	57%	0.0	100%
AB293445.1	Saccharomyces cerevisiae gene for aquaporin Aqy1, complete cds, clone: COS4	1471	1471	57%	0.0	100%
FM162567.1	Trypanosoma brucei Lister 427 surface glycoprotein expression site BES2/TAR129, from bloodstream	1471	1471	57%	0.0	100%
EU491017.1	Suicide vector pEX18Km-pheS, complete sequence	1471	1471	57%	0.0	100%
EU232662.1	Cloning vector pVMGCRT85, complete sequence	1471	1471	57%	0.0	100%
EU232661.1	Cloning vector pVMG-TnpR, complete sequence	1471	1471	57%	0.0	100%
AB366441.1	Salmonella enterica subsp. enterica serovar Dublin plasmid pMAK2 DNA, complete genome, strain: L-789	1471	1471	57%	0.0	100%
EU047752.1	Cloning vector pDC8, complete sequence	1471	2177	57%	0.0	100%
EU024548.1	Cloning vector pCPP5250, complete sequence	1471	1471	57%	0.0	100%
EU024546.1	Cloning vector pCPP5702, complete sequence	1471	1471	57%	0.0	100%
EF437956.1	Expression vector pcDNA3-AQP4f, complete sequence	1471	1471	57%	0.0	100%
EF437953.1	Expression vector pcDNA3-AQP4e, complete sequence	1471	1471	57%	0.0	100%
EF437951.1	Expression vector pcDNA3-AQP4d, complete sequence	1471	1471	57%	0.0	100%
EF437950.1		1471	1471	57%	0.0	100%

	Expression vector pcDNA3-K-AQP4d, complete sequence					
CP000744.1	Pseudomonas aeruginosa PA7, complete genome	1471	1471	57%	0.0	100%
AY667410.1	Shuttle cosmid vector pHZ1358, complete sequence	1471	1471	57%	0.0	100%
AM711972.1	Transposon mutagenesis vector pMiET	1471	1471	57%	0.0	100%
EF550208.1	Cloning vector pcDNA3.1+PA, complete sequence	1471	1471	57%	0.0	100%
EF192606.1	Cloning vector pBEO210, complete sequence	1471	1471	57%	0.0	100%
EF028675.1	Cloning vector pDV-NTAP-CYFP, complete sequence	1471	1471	57%	0.0	100%
EF028674.1	Cloning vector pDV-NTAP-CGFP, complete sequence	1471	1471	57%	0.0	100%
EF028673.1	Cloning vector pDV-CYFP-CTAP, complete sequence	1471	1471	57%	0.0	100%
EF028672.1	Cloning vector pDV-CGFP-CTAP, complete sequence	1471	1471	57%	0.0	100%
EF028671.1	Cloning vector pDV-NYFP-CTAP, complete sequence	1471	1471	57%	0.0	100%
EF028670.1	Cloning vector pDV-NTAP-NYFP, complete sequence	1471	1471	57%	0.0	100%
EF028669.1	Cloning vector pDV-CTAP, complete sequence	1471	1471	57%	0.0	100%
EF028668.1	Cloning vector pDV-CYFP, complete sequence	1471	1471	57%	0.0	100%
EF028667.1	Cloning vector pDV-CGFP, complete sequence	1471	1471	57%	0.0	100%
EF028666.1	Cloning vector pDV-NTAP, complete sequence	1471	1471	57%	0.0	100%
EF028665.1	Cloning vector pDV-NYFP, complete sequence	1471	1471	57%	0.0	100%
EF028664.1	Cloning vector EXP5(+), complete sequence	1471	1471	57%	0.0	100%
EF028663.1	Cloning vector EXP4(+), complete sequence	1471	1471	57%	0.0	100%
EF177812.1	Expression vector pUNIV, complete sequence	1471	1471	57%	0.0	100%
EF030522.1	Inducible protein expression vector pReg Neo, complete sequence	1471	1471	57%	0.0	100%
AB255435.1	Escherichia coli plasmid pO86A1 DNA, complete sequence	1471	1471	57%	0.0	100%
DQ886588.1	Expression vector pcDNA3-hFIX, complete sequence	1471	1471	57%	0.0	100%
DQ898181.1	Keratinocyte expression vector phPK14H, complete sequence	1471	1471	57%	0.0	100%
DQ823233.1	Expression vector mce4, complete sequence	1471	1471	57%	0.0	100%
DQ823232.1	Expression vector mce3, complete sequence	1471	1471	57%	0.0	100%
DQ823231.1	Expression vector mce2, complete sequence	1471	1471	57%	0.0	100%
DQ487156.1	Flexi vector pF5K CMV-neo, complete sequence	1471	1471	57%	0.0	100%
DQ487155.1	Flexi vector pF5A CMV-neo, complete sequence	1471	1471	57%	0.0	100%
DQ487211.1	Flexi Vector pFN10A (ACT), complete sequence	1471	1471	57%	0.0	100%
DQ515893.1	HIS3/URA3 reporter vector pH3U3, complete sequence	1471	1471	57%	0.0	100%
DQ408591.1	Transposon mutagenesis vector pG18-STM, complete sequence	1471	1471	57%	0.0	100%
AY817672.1	SIV vector pCLN8, complete sequence	1471	1471	57%	0.0	100%
AY266291.1	Escherichia coli/Mycobacteria shuttle vector pGB9.2, complete sequence	1471	1471	57%	0.0	100%
AY613997.1	Cloning vector pSRalphaneoR, complete sequence	1471	3585	99%	0.0	100%

AY613992.1	Cloning vector pSRalphaneo, complete sequence	1471	1471	57%	0.0	100%
AY286001.1	Cloning vector pHRE1-km, complete sequence	1471	1471	57%	0.0	100%
DQ059989.1	Cloning vector pSCR001, complete sequence	1471	1471	57%	0.0	100%
AY260554.1	Retrotransposon vector MEL/ELM, complete sequence	1471	2495	98%	0.0	100%
AY260553.1	Retrotransposon vector ELM 5, complete sequence	1471	2495	98%	0.0	100%
AY037297.1	Synthetic construct erythromycin resistance protein (erm) gene, partial cds; and streptomycin 3'-phosphotransferase (sph), bleomycin phosphotransferase (ble), neomycin phosphotransferase (nptII), and gentamycin resistance protein (aac) genes, complete cds	1471	1471	57%	0.0	100%
AF264696.2	Cloning vector pFB-ERV, complete sequence	1471	3430	99%	0.0	100%
DQ092437.1	Insertion vector pWSMK-T, complete sequence	1471	1471	57%	0.0	100%
AF504908.1	Cloning vector pBBRT, complete sequence	1471	1471	57%	0.0	100%
AY062236.1	Transformation vector pRLE6, complete sequence	1471	1471	57%	0.0	100%
AF416990.1	Synthetic construct plasmid pcDNA3-Rluc, complete sequence	1471	1471	57%	0.0	100%
AY181092.1	Synthetic construct S1 promoter-nptII gene-S3 terminator cassette	1471	1471	57%	0.0	100%
AY159034.1	Cloning vector pPLEX-4004, complete sequence	1471	1471	57%	0.0	100%
AY159033.1	Cloning vector pPLEX-4003, complete sequence	1471	1471	57%	0.0	100%
AY159032.1	Cloning vector pPLEX-4002, complete sequence	1471	1471	57%	0.0	100%
AY159031.1	Cloning vector pPLEX-4001, complete sequence	1471	1471	57%	0.0	100%
AY159029.1	Cloning vector pPLEX-501, complete sequence	1471	1471	57%	0.0	100%
AY159020.1	Cloning vector pPLEX-505, complete sequence	1471	1471	57%	0.0	100%
AY048743.1	Template plasmid pKD4, complete sequence	1471	1471	57%	0.0	100%
AY237648.1	Cloning vector pHR50, complete sequence	1471	1471	57%	0.0	100%
AY237649.1	Cloning vector pHR3-km, complete sequence	1471	1471	57%	0.0	100%
AY265466.1	Shuttle vector pAM2770, complete sequence	1471	1471	57%	0.0	100%
AF346624.1	RAGE vector pRIG1, complete sequence	1471	1471	57%	0.0	100%
AL671256.1	Trypanosoma brucei VO2 VSG expression site BAC	1471	1471	57%	0.0	100%
AF286462.1	Promoter probe vector pPROBE'-gfp[LVA], complete sequence	1471	1471	57%	0.0	100%
AF286461.1	Promoter probe vector pPROBE-gfp[LVA], complete sequence	1471	1471	57%	0.0	100%
AF286460.1	Promoter probe vector pPROBE'-gfp[ASV], complete sequence	1471	1471	57%	0.0	100%
AF286459.1	Promoter probe vector pPROBE-gfp[ASV], complete sequence	1471	1471	57%	0.0	100%
AF286458.1	Promoter probe vector pPROBE'-gfp[AAV], complete sequence	1471	1471	57%	0.0	100%
AF286457.1	Promoter probe vector pPROBE-gfp[AAV], complete sequence	1471	1471	57%	0.0	100%
AF286456.1	Promoter probe vector pPROBE'-gfp[tagless], complete sequence	1471	1471	57%	0.0	100%
AF286455.1	Promoter probe vector pPROBE-gfp[tagless], complete sequence	1471	1471	57%	0.0	100%
AF286454.1	Promoter probe vector pPROBE-NT', complete	1471	1471	57%	0.0	100%

	sequence				
AF286453.1	Promoter probe vector pPROBE-NT, complete sequence	1471	1471	57%	0.0	100%
AY962288.1	Low threshold vector pLTSUB-302, complete sequence	1471	1471	57%	0.0	100%
AY952935.1	Expression vector pFNK-101, complete sequence	1471	1471	57%	0.0	100%
AY952936.1	Expression vector pINV-110, complete sequence	1471	1471	57%	0.0	100%
DQ225747.1	Gene trapping Ds/T-DNA vector pUR224NB, complete sequence	1471	1471	57%	0.0	100%
DQ225746.1	Gene trapping Ds/T-DNA vector pUR224NA, complete sequence	1471	1471	57%	0.0	100%

Alignments Select All Get selected sequences Distance tree of results

>dbj|AB237837.1| Hepatitis C virus full-length replicon pFGR-JFH1 RNA, complet
sequence
Length=11111

 Score = 2542 bits (1376), Expect = 0.0
 Identities = 1376/1376 (100%), Gaps = 0/1376 (0%)
 Strand=Plus/Plus

Query 398   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC 457
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 398   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC 457

Query 458   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA 517
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 458   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA 517

Query 518   GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG 577
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 518   GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG 577

Query 578   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG 637
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 578   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG 637

Query 638   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG 697
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 638   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG 697

Query 698   GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG 757
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 698   GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG 757

Query 758   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC 817
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 758   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC 817

Query 818   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA 877
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 818   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA 877

Query 878   GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC 937
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 878   GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC 937

Query 938   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT 997
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 938   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT 997

Query 998   GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 1057
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 998   GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 1057

Query 1058 ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC 1117
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1058 ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC 1117

Query 1118 CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT 1177
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Sbjct  1118  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT  1177

Query  1178  GACGAGTTCTTCTGAGTTTAAACCCTCTCCCTccccccccccTAACGTTACTGGCCGAAG  1237
             ||||||||||||||||||||||||||||||||           ||||||||||||||||||
Sbjct  1178  GACGAGTTCTTCTGAGTTTAAACCCTCTCCCTCCCCCCCCCCTAACGTTACTGGCCGAAG  1237

Query  1238  CCGCTTGGAATAAGGCCGGTGTGCGTTTGTCTATATGTTATTTTCCACCATATTGCCGTC  1297
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Query  1298  TTTTGGCAATGTGAGGGCCCGGAAACCTGGCCCTGTCTTCTTGACGAGCATTCCTAGGGG  1357
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Query  1358  TCTTTCCCCTCTCGCCAAAGGAATGCAAGGTCTGTTGAATGTCGTGAAGGAAGCAGTTCC  1417
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Sbjct  1358  TCTTTCCCCTCTCGCCAAAGGAATGCAAGGTCTGTTGAATGTCGTGAAGGAAGCAGTTCC  1417

Query  1418  TCTGGAAGCTTCTTGAAGACAAACAACGTCTGTAGCGACCCTTTGCAGGCAGCGGAACCC  1477
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Query  1478  CCCACCTGGCGACAGGTGCCTCTGCGGCCAAAAGCCACGTGTATAAGATACACCTGCAAA  1537
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1478  CCCACCTGGCGACAGGTGCCTCTGCGGCCAAAAGCCACGTGTATAAGATACACCTGCAAA  1537

Query  1538  GGCGGCACAACCCCAGTGCCACGTTGTGAGTTGGATAGTTGTGGAAAGAGTCAAATGGCT  1597
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1538  GGCGGCACAACCCCAGTGCCACGTTGTGAGTTGGATAGTTGTGGAAAGAGTCAAATGGCT  1597

Query  1598  CTCCTCAAGCGTATTCAACAAGGGGCTGAAGGATGCCCAGAAGGTACCCCATTGTATGGG  1657
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1598  CTCCTCAAGCGTATTCAACAAGGGGCTGAAGGATGCCCAGAAGGTACCCCATTGTATGGG  1657

Query  1658  ATCTGATCTGGGGCCTCGGTGCACATGCTTTACATGTGTTTAGTCGAGGTTaaaaaaaCG  1717
             |||||||||||||||||||||||||||||||||||||||||||||||||||       ||
Sbjct  1658  ATCTGATCTGGGGCCTCGGTGCACATGCTTTACATGTGTTTAGTCGAGGTTAAAAAAACG  1717

Query  1718  TCTAGGCCCCCCGAACCACGGGGACGTGGTTTTCCTTTGAAAAACACGATGATACC  1773
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1718  TCTAGGCCCCCCGAACCACGGGGACGTGGTTTTCCTTTGAAAAACACGATGATACC  1773
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>dbj|AB114136.1| Hepatitis C virus replicon pSGR-JFH1 gene for neomysin resistan
gene product, hepatitis C virus nonstructural protein,
complete cds
Length=8024

 Score = 2542 bits (1376), Expect = 0.0
 Identities = 1376/1376 (100%), Gaps = 0/1376 (0%)
 Strand=Plus/Plus

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Query  398  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC  457
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Query  458  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA  517
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Sbjct  458  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA  517

Query  518  GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG  577
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  518  GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG  577

Query  578  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG  637
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Query  638  CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG  697
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Query  698  GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG  757
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  698  GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG  757

Query  758  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC  817
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  758  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC  817
```

```
Query   818   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   877
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   818   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   877

Query   878   GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   937
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   878   GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   937

Query   938   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   997
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Sbjct   938   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   997

Query   998   GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   1057
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   998   GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   1057

Query   1058  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   1117
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1058  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   1117

Query   1118  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   1177
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Sbjct   1118  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   1177

Query   1178  GACGAGTTCTTCTGAGTTTAAACCCTCTCCCTccccccccccTAACGTTACTGGCCGAAG   1237
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Sbjct   1178  GACGAGTTCTTCTGAGTTTAAACCCTCTCCCTCCCCCCCCCCCTAACGTTACTGGCCGAAG   1237

Query   1238  CCGCTTGGAATAAGGCCGGTGTGCGTTTGTCTATATGTTATTTTCCACCATATTGCCGTC   1297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1238  CCGCTTGGAATAAGGCCGGTGTGCGTTTGTCTATATGTTATTTTCCACCATATTGCCGTC   1297

Query   1298  TTTTGGCAATGTGAGGGCCCGGAAACCTGGCCCTGTCTTCTTGACGAGCATTCCTAGGGG   1357
              ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Sbjct   1298  TTTTGGCAATGTGAGGGCCCGGAAACCTGGCCCTGTCTTCTTGACGAGCATTCCTAGGGG   1357

Query   1358  TCTTTCCCCTCTCGCCAAAGGAATGCAAGGTCTGTTGAATGTCGTGAAGGAAGCAGTTCC   1417
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Sbjct   1358  TCTTTCCCCTCTCGCCAAAGGAATGCAAGGTCTGTTGAATGTCGTGAAGGAAGCAGTTCC   1417

Query   1418  TCTGGAAGCTTCTTGAAGACAAACAACGTCTGTAGCGACCCTTTGCAGGCAGCGGAACCC   1477
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1418  TCTGGAAGCTTCTTGAAGACAAACAACGTCTGTAGCGACCCTTTGCAGGCAGCGGAACCC   1477

Query   1478  CCCACCTGGCGACAGGTGCCTCTGCGGCCAAAAGCCACGTGTATAAGATACACCTGCAAA   1537
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1478  CCCACCTGGCGACAGGTGCCTCTGCGGCCAAAAGCCACGTGTATAAGATACACCTGCAAA   1537

Query   1538  GGCGGCACAACCCCAGTGCCACGTTGTGAGTTGGATAGTTGTGGAAAGAGTCAAATGGCT   1597
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Sbjct   1538  GGCGGCACAACCCCAGTGCCACGTTGTGAGTTGGATAGTTGTGGAAAGAGTCAAATGGCT   1597

Query   1598  CTCCTCAAGCGTATTCAACAAGGGGCTGAAGGATGCCCAGAAGGTACCCCATTGTATGGG   1657
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Sbjct   1598  CTCCTCAAGCGTATTCAACAAGGGGCTGAAGGATGCCCAGAAGGTACCCCATTGTATGGG   1657

Query   1658  ATCTGATCTGGGGCCTCGGTGCACATGCTTTACATGTGTTTAGTCGAGGTTaaaaaaaCG   1717
              |||||||||||||||||||||||||||||||||||||||||||||||||||          ||
Sbjct   1658  ATCTGATCTGGGGCCTCGGTGCACATGCTTTACATGTGTTTAGTCGAGGTTAAAAAAACG   1717

Query   1718  TCTAGGCCCCCCGAACCACGGGGACGTGGTTTTCCTTTGAAAAACACGATGATACC     1773
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1718  TCTAGGCCCCCCGAACCACGGGGACGTGGTTTTCCTTTGAAAAACACGATGATACC     1773
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>gb|AF311318.1|AF311318   Retroviral vector NIT, complete sequence
Length=7607

 Score = 2390 bits (1294),   Expect = 0.0
 Identities = 1370/1401 (97%), Gaps = 28/1401 (1%)
 Strand=Plus/Plus

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Query   398   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   457
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Sbjct   1686  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   1745

Query   458   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   517
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1746  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   1805
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Query   518    GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   577
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1806   GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   1865

Query   578    CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   637
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1866   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   1925

Query   638    CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   697
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1926   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   1985

Query   698    GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   757
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1986   GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   2045

Query   758    CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   817
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2046   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   2105

Query   818    ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   877
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2106   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   2165

Query   878    GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   937
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2166   GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   2225

Query   938    GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   997
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2226   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   2285

Query   998    GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   1057
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2286   GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   2345

Query   1058   ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   1117
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2346   ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   2405

Query   1118   CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   1177
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2406   CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   2465

Query   1178   GACGAGTTCTTCTGAG------T-T----T------AAAC-----CCTCTCC-CTcccc-c   1213
               ||||||||||||||||       | |     |        ||||       || | || |||||| |
Sbjct   2466   GACGAGTTCTTCTGAGCGGGACTCTGGGGTTCGGTTAAACGAATTCCGCCCCTCTCCCTC   2525

Query   1214   cccccc---TAACGTTACTGGCCGAAGCCGCTTGGAATAAGGCCGGTGTGCGTTTGTCTA   1270
               ||||||       |||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2526   CCCCCCCCCTAACGTTACTGGCCGAAGCCGCTTGGAATAAGGCCGGTGTGCGTTTGTCTA   2585

Query   1271   TATGTTATTTTCCACCATATTGCCGTCTTTTGGCAATGTGAGGGCCCGGAAACCTGGCCC   1330
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2586   TATGTTATTTTCCACCATATTGCCGTCTTTTGGCAATGTGAGGGCCCGGAAACCTGGCCC   2645

Query   1331   TGTCTTCTTGACGAGCATTCCTAGGGGTCTTTCCCCTCTCGCCAAAGGAATGCAAGGTCT   1390
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2646   TGTCTTCTTGACGAGCATTCCTAGGGGTCTTTCCCCTCTCGCCAAAGGAATGCAAGGTCT   2705

Query   1391   GTTGAATGTCGTGAAGGAAGCAGTTCCTCTGGAAGCTTCTTGAAGACAAACAACGTCTGT   1450
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2706   GTTGAATGTCGTGAAGGAAGCAGTTCCTCTGGAAGCTTCTTGAAGACAAACAACGTCTGT   2765

Query   1451   AGCGACCCTTTGCAGGCAGCGGAACCCCCCACCTGGCGACAGGTGCCTCTGCGGCCAAAA   1510
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2766   AGCGACCCTTTGCAGGCAGCGGAACCCCCCACCTGGCGACAGGTGCCTCTGCGGCCAAAA   2825

Query   1511   GCCACGTGTATAAGATACACCTGCAAAGGCGGCACAACCCCAGTGCCACGTTGTGAGTTG   1570
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2826   GCCACGTGTATAAGATACACCTGCAAAGGCGGCACAACCCCAGTGCCACGTTGTGAGTTG   2885

Query   1571   GATAGTTGTGGAAAGAGTCAAATGGCTCTCCTCAAGCGTATTCAACAAGGGGCTGAAGGA   1630
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2886   GATAGTTGTGGAAAGAGTCAAATGGCTCTCCTCAAGCGTATTCAACAAGGGGCTGAAGGA   2945

Query   1631   TGCCCAGAAGGTACCCCATTGTATGGGATCTGATCTGGGGCCTCGGTGCACATGCTTTAC   1690
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2946   TGCCCAGAAGGTACCCCATTGTATGGGATCTGATCTGGGGCCTCGGTGCACATGCTTTAC   3005
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Query   1691   ATGTGTTTAGTCGAGGTTaaaaaaCGTCTAGGCCCCCCGAACCACGGGGACGTGGTTTT   1750
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Sbjct   3006   GTGTGTTTAGTCGAGGTTAAAAAA-CGTCTAGGCCCCCCGAACCACGGGGACGTGGTTTT   3064

Query   1751   CCTTTGAAAAACACGATGATA   1771
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Sbjct   3065   CCTTTGAAAAACACGATGATA   3085
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>dbj|AB119282.1| Hepatitis C virus gene for Fusion protein, Feo, complete cds
Length=9658

Score = 1483 bits (803), Expect = 0.0
Identities = 803/803 (100%), Gaps = 0/803 (0%)
Strand=Plus/Plus

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Query   398    ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   457
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Sbjct   2046   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   2105

Query   458    GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   517
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2106   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   2165

Query   518    GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   577
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2166   GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   2225

Query   578    CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   637
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Sbjct   2226   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   2285

Query   638    CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   697
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2286   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   2345

Query   698    GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   757
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2346   GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   2405

Query   758    CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   817
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2406   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   2465

Query   818    ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   877
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Sbjct   2466   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   2525

Query   878    GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   937
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Sbjct   2526   GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   2585

Query   938    GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   997
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2586   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   2645

Query   998    GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   1057
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Sbjct   2646   GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   2705

Query   1058   ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   1117
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Sbjct   2706   ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   2765

Query   1118   CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   1177
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2766   CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   2825

Query   1178   GACGAGTTCTTCTGAGTTTAAAC   1200
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Sbjct   2826   GACGAGTTCTTCTGAGTTTAAAC   2848
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Score = 1048 bits (567), Expect = 0.0
Identities = 572/574 (99%), Gaps = 1/574 (0%)
Strand=Plus/Plus

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Query  1200  CCCTCTCCCTccccccccccTAACGTTACTGGCCGAAGCCGCTTGGAATAAGGCCGGTGT  1259
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Sbjct  2887  CCCTCTCCCTCCCCCCCCCCTAACGTTACTGGCCGAAGCCGCTTGGAATAAGGCCGGTGT  2946

Query  1260  GCGTTTGTCTATATGTTATTTTCCACCATATTGCCGTCTTTTGGCAATGTGAGGGCCCGG  1319
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2947  GCGTTTGTCTATATGTTATTTTCCACCATATTGCCGTCTTTTGGCAATGTGAGGGCCCGG  3006

Query  1320  AAACCTGGCCCTGTCTTCTTGACGAGCATTCCTAGGGGTCTTTCCCCTCTCGCCAAAGGA  1379
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3007  AAACCTGGCCCTGTCTTCTTGACGAGCATTCCTAGGGGTCTTTCCCCTCTCGCCAAAGGA  3066

Query  1380  ATGCAAGGTCTGTTGAATGTCGTGAAGGAAGCAGTTCCTCTGGAAGCTTCTTGAAGACAA  1439
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Sbjct  3067  ATGCAAGGTCTGTTGAATGTCGTGAAGGAAGCAGTTCCTCTGGAAGCTTCTTGAAGACAA  3126

Query  1440  ACAACGTCTGTAGCGACCCTTTGCAGGCAGCGGAACCCCCCACCTGGCGACAGGTGCCTC  1499
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Sbjct  3127  ACAACGTCTGTAGCGACCCTTTGCAGGCAGCGGAACCCCCCACCTGGCGACAGGTGCCTC  3186

Query  1500  TGCGGCCAAAAGCCACGTGTATAAGATACACCTGCAAAGGCGGCACAACCCCAGTGCCAC  1559
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3187  TGCGGCCAAAAGCCACGTGTATAAGATACACCTGCAAAGGCGGCACAACCCCAGTGCCAC  3246

Query  1560  GTTGTGAGTTGGATAGTTGTGGAAAGAGTCAAATGGCTCTCCTCAAGCGTATTCAACAAG  1619
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3247  GTTGTGAGTTGGATAGTTGTGGAAAGAGTCAAATGGCTCTCCTCAAGCGTATTCAACAAG  3306

Query  1620  GGGCTGAAGGATGCCCAGAAGGTACCCCATTGTATGGGATCTGATCTGGGGCCTCGGTGC  1679
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Sbjct  3307  GGGCTGAAGGATGCCCAGAAGGTACCCCATTGTATGGGATCTGATCTGGGGCCTCGGTGC  3366

Query  1680  ACATGCTTTACATGTGTTTAGTCGAGGTTaaaaaaaCGTCTAGGCCCCCCGAACCACGGG  1739
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Sbjct  3367  ACATGCTTTACATGTGTTTAGTCGAGGTTAAAAAA-CGTCTAGGCCCCCCGAACCACGGG  3425

Query  1740  GACGTGGTTTTCCTTTGAAAAACACGATGATACC     1773
             |||||||||||||||||||||||||||||| |||||
Sbjct  3426  GACGTGGTTTTCCTTTGAAAAACACGATAATACC     3459


>gb|DQ320121.1| ▨ Binary vector pBINPLUS/ARS, complete sequence
Length=12460

 Score = 1483 bits (803),  Expect = 0.0
 Identities = 803/803 (100%), Gaps = 0/803 (0%)
 Strand=Plus/Plus

Query  398   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC  457
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Sbjct  7952  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC  8011

Query  458   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA  517
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  8012  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA  8071

Query  518   GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG  577
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Sbjct  8072  GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG  8131

Query  578   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG  637
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Sbjct  8132  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG  8191

Query  638   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG  697
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  8192  CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG  8251

Query  698   GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG  757
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  8252  GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG  8311

Query  758   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC  817
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Sbjct  8312  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC  8371

Query  818   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA  877
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Sbjct  8372   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA  8431

Query  878    GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC  937
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  8432   GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC  8491

Query  938    GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT  997
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  8492   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT  8551

Query  998    GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC  1057
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Sbjct  8552   GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC  8611

Query  1058   ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC  1117
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  8612   ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC  8671

Query  1118   CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT  1177
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Sbjct  8672   CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT  8731

Query  1178   GACGAGTTCTTCTGAGTTTAAAC   1200
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>emb|AJ242651.1|SSE242651   Hepatitis C virus replicon I377/NS2-3'UTR
Length=8637
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                                              Sort alignments for this
                                                E value   Score   Percen
                                              Query start position

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 Score = 1483 bits (803),  Expect = 0.0
 Identities = 803/803 (100%), Gaps = 0/803 (0%)
 Strand=Plus/Plus

Query  398    ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC  457
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Sbjct  387    ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC  446

Query  458    GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA  517
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Sbjct  447    GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA  506

Query  518    GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG  577
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  507    GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG  566

Query  578    CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG  637
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Sbjct  567    CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG  626

Query  638    CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG  697
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Sbjct  627    CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG  686

Query  698    GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG  757
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Sbjct  687    GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG  746

Query  758    CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC  817
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Sbjct  747    CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC  806

Query  818    ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA  877
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Sbjct  807    ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA  866

Query  878    GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC  937
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Sbjct  867    GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC  926

Query  938    GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT  997
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Sbjct  927    GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT  986

Query  998    GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC  1057
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Sbjct   987   GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   1046

Query  1058   ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   1117
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Sbjct  1047   ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   1106

Query  1118   CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   1177
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Sbjct  1107   CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   1166

Query  1178   GACGAGTTCTTCTGAGTTTAAAC    1200
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Sbjct  1167   GACGAGTTCTTCTGAGTTTAAAC    1189


 Score = 1048 bits (567),   Expect = 0.0
 Identities = 572/574 (99%), Gaps = 1/574 (0%)
 Strand=Plus/Plus

Query  1200   CCCTCTCCCTccccccccccccTAACGTTACTGGCCGAAGCCGCTTGGAATAAGGCCGGTGT   1259
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Sbjct  1228   CCCTCTCCCTCCCCCCCCCCCTAACGTTACTGGCCGAAGCCGCTTGGAATAAGGCCGGTGT   1287

Query  1260   GCGTTTGTCTATATGTTATTTTCCACCATATTGCCGTCTTTTGGCAATGTGAGGGCCCGG   1319
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1288   GCGTTTGTCTATATGTTATTTTCCACCATATTGCCGTCTTTTGGCAATGTGAGGGCCCGG   1347

Query  1320   AAACCTGGCCCTGTCTTCTTGACGAGCATTCCTAGGGGTCTTTCCCCTCTCGCCAAAGGA   1379
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Sbjct  1348   AAACCTGGCCCTGTCTTCTTGACGAGCATTCCTAGGGGTCTTTCCCCTCTCGCCAAAGGA   1407

Query  1380   ATGCAAGGTCTGTTGAATGTCGTGAAGGAAGCAGTTCCTCTGGAAGCTTCTTGAAGACAA   1439
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1408   ATGCAAGGTCTGTTGAATGTCGTGAAGGAAGCAGTTCCTCTGGAAGCTTCTTGAAGACAA   1467

Query  1440   ACAACGTCTGTAGCGACCCTTTGCAGGCAGCGGAACCCCCCACCTGGCGACAGGTGCCTC   1499
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Sbjct  1468   ACAACGTCTGTAGCGACCCTTTGCAGGCAGCGGAACCCCCCACCTGGCGACAGGTGCCTC   1527

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Query  1560   GTTGTGAGTTGGATAGTTGTGGAAAGAGTCAAATGGCTCTCCTCAAGCGTATTCAACAAG   1619
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Sbjct  1588   GTTGTGAGTTGGATAGTTGTGGAAAGAGTCAAATGGCTCTCCTCAAGCGTATTCAACAAG   1647

Query  1620   GGGCTGAAGGATGCCCAGAAGGTACCCCATTGTATGGGATCTGATCTGGGGCCTCGGTGC   1679
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1648   GGGCTGAAGGATGCCCAGAAGGTACCCCATTGTATGGGATCTGATCTGGGGCCTCGGTGC   1707

Query  1680   ACATGCTTTACATGTGTTTAGTCGAGGTTaaaaaaaCGTCTAGGCCCCCCGAACCACGGG   1739
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Sbjct  1708   ACATGCTTTACATGTGTTTAGTCGAGGTTAAAAAA-CGTCTAGGCCCCCCGAACCACGGG   1766

Query  1740   GACGTGGTTTTCCTTTGAAAAACACGATGATACC     1773
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>emb|AJ242654.1|SSE242654   Hepatitis C virus replicon I389/NS3-3'UTR
Length=8001
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 Score = 1483 bits (803),   Expect = 0.0
 Identities = 803/803 (100%), Gaps = 0/803 (0%)
 Strand=Plus/Plus

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Sbjct   399   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   458

Query   458   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   517
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Sbjct   459   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   518

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Sbjct  519   GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   578

Query  578   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   637
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Sbjct  579   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   638

Query  638   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   697
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Sbjct  639   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   698

Query  698   GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   757
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Sbjct  699   GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   758

Query  758   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   817
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Sbjct  759   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   818

Query  818   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   877
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Sbjct  819   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   878

Query  878   GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   937
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Query  998   GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   1057
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Sbjct  999   GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   1058

Query  1058  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   1117
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Query  1118  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   1177
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Sbjct  1119  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   1178

Query  1178  GACGAGTTCTTCTGAGTTTAAAC       1200
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Sbjct  1179  GACGAGTTCTTCTGAGTTTAAAC       1201
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  Score = 1048 bits (567),   Expect = 0.0
  Identities = 572/574 (99%), Gaps = 1/574 (0%)
  Strand=Plus/Plus
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Sbjct  1240  CCCTCTCCCTCCCCCCCCCCTAACGTTACTGGCCGAAGCCGCTTGGAATAAGGCCGGTGT   1299

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Sbjct  1300  GCGTTTGTCTATATGTTATTTTCCACCATATTGCCGTCTTTTGGCAATGTGAGGGCCCGG   1359

Query  1320  AAACCTGGCCCTGTCTTCTTGACGAGCATTCCTAGGGGTCTTTCCCCTCTCGCCAAAGGA   1379
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Sbjct  1360  AAACCTGGCCCTGTCTTCTTGACGAGCATTCCTAGGGGTCTTTCCCCTCTCGCCAAAGGA   1419

Query  1380  ATGCAAGGTCTGTTGAATGTCGTGAAGGAAGCAGTTCCTCTGGAAGCTTCTTGAAGACAA   1439
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Sbjct  1420  ATGCAAGGTCTGTTGAATGTCGTGAAGGAAGCAGTTCCTCTGGAAGCTTCTTGAAGACAA   1479

Query  1440  ACAACGTCTGTAGCGACCCTTTGCAGGCAGCGGAACCCCCCACCTGGCGACAGGTGCCTC   1499
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Query  1560  GTTGTGAGTTGGATAGTTGTGGAAAGAGTCAAATGGCTCTCCTCAAGCGTATTCAACAAG   1619
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Query  1620  GGGCTGAAGGATGCCCAGAAGGTACCCCATTGTATGGGATCTGATCTGGGGCCTCGGTGC  1679
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Sbjct  1660  GGGCTGAAGGATGCCCAGAAGGTACCCCATTGTATGGGATCTGATCTGGGGCCTCGGTGC  1719

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Query  1740  GACGTGGTTTTCCTTTGAAAAACACGATGATACC     1773
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>emb|AJ242653.1|SSE242653   Hepatitis C virus replicon I389/NS2-3'UTR
Length=8649

Sort alignments for this
E value   Score   Percen
Query start position

Score = 1483 bits (803),   Expect = 0.0
Identities = 803/803 (100%), Gaps = 0/803 (0%)
Strand=Plus/Plus

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Query  398   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC  457
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Query  578   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG  637
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Query  758   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC  817
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  759   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC  818

Query  818   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA  877
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Sbjct  999   GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC  1058

Query  1058  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC  1117
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Query  1118  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT  1177
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Sbjct  1119  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT  1178

Query  1178  GACGAGTTCTTCTGAGTTTAAAC     1200
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Sbjct  1179  GACGAGTTCTTCTGAGTTTAAAC     1201
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Score = 1048 bits (567),  Expect = 0.0
Identities = 572/574 (99%), Gaps = 1/574 (0%)
Strand=Plus/Plus

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Query  1320  AAACCTGGCCCTGTCTTCTTGACGAGCATTCCTAGGGGTCTTTCCCCTCTCGCCAAAGGA  1379
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Sbjct  1600  GTTGTGAGTTGGATAGTTGTGGAAAGAGTCAAATGGCTCTCCTCAAGCGTATTCAACAAG  1659

Query  1620  GGGCTGAAGGATGCCCAGAAGGTACCCCATTGTATGGGATCTGATCTGGGGCCTCGGTGC  1679
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1660  GGGCTGAAGGATGCCCAGAAGGTACCCCATTGTATGGGATCTGATCTGGGGCCTCGGTGC  1719

Query  1680  ACATGCTTTACATGTGTTTAGTCGAGGTTaaaaaaaCGTCTAGGCCCCCCGAACCACGGG  1739
             |||||||||||||||||||||||||||||        |||||||||||||||||||||||
Sbjct  1720  ACATGCTTTACATGTGTTTAGTCGAGGTTAAAAAA-CGTCTAGGCCCCCCGAACCACGGG  1778

Query  1740  GACGTGGTTTTCCTTTGAAAAACACGATGATACC    1773
             |||||||||||||||||||||||||||||| |||||
Sbjct  1779  GACGTGGTTTTCCTTTGAAAAACACGATAATACC    1812


>emb|AJ242652.1|SSE242652  Hepatitis C virus replicon I377/NS3-3'UTR
Length=7989
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Score = 1483 bits (803),  Expect = 0.0
Identities = 803/803 (100%), Gaps = 0/803 (0%)
Strand=Plus/Plus

Query  398  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC  457
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  387  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC  446

Query  458  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA  517
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  447  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA  506

Query  518  GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG  577
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  507  GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG  566

Query  578  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG  637
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  567  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG  626

Query  638  CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG  697
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  627  CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG  686

Query  698  GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG  757
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  687  GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG  746
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Query   758   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   817
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   747   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   806

Query   818   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   877
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   807   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   866

Query   878   GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   937
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   867   GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   926

Query   938   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   997
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   927   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   986

Query   998   GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   1057
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   987   GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   1046

Query   1058  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   1117
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1047  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   1106

Query   1118  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   1177
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1107  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   1166

Query   1178  GACGAGTTCTTCTGAGTTTAAAC    1200
              |||||||||||||||||||||||
Sbjct   1167  GACGAGTTCTTCTGAGTTTAAAC    1189


 Score = 1048 bits (567),  Expect = 0.0
 Identities = 572/574 (99%), Gaps = 1/574 (0%)
 Strand=Plus/Plus

Query   1200  CCCTCTCCCTccccccccccccTAACGTTACTGGCCGAAGCCGCTTGGAATAAGGCCGGTGT   1259
              |||||||||||                    |||||||||||||||||||||||||||||||
Sbjct   1228  CCCTCTCCCTCCCCCCCCCCCTAACGTTACTGGCCGAAGCCGCTTGGAATAAGGCCGGTGT   1287

Query   1260  GCGTTTGTCTATATGTTATTTTCCACCATATTGCCGTCTTTTGGCAATGTGAGGGCCCGG   1319
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1288  GCGTTTGTCTATATGTTATTTTCCACCATATTGCCGTCTTTTGGCAATGTGAGGGCCCGG   1347

Query   1320  AAACCTGGCCCTGTCTTCTTGACGAGCATTCCTAGGGGTCTTTCCCCTCTCGCCAAAGGA   1379
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1348  AAACCTGGCCCTGTCTTCTTGACGAGCATTCCTAGGGGTCTTTCCCCTCTCGCCAAAGGA   1407

Query   1380  ATGCAAGGTCTGTTGAATGTCGTGAAGGAAGCAGTTCCTCTGGAAGCTTCTTGAAGACAA   1439
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1408  ATGCAAGGTCTGTTGAATGTCGTGAAGGAAGCAGTTCCTCTGGAAGCTTCTTGAAGACAA   1467

Query   1440  ACAACGTCTGTAGCGACCCTTTGCAGGCAGCGGAACCCCCCACCTGGCGACAGGTGCCTC   1499
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1468  ACAACGTCTGTAGCGACCCTTTGCAGGCAGCGGAACCCCCCACCTGGCGACAGGTGCCTC   1527

Query   1500  TGCGGCCAAAAGCCACGTGTATAAGATACACCTGCAAAGGCGGCACAACCCCAGTGCCAC   1559
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1528  TGCGGCCAAAAGCCACGTGTATAAGATACACCTGCAAAGGCGGCACAACCCCAGTGCCAC   1587

Query   1560  GTTGTGAGTTGGATAGTTGTGGAAAGAGTCAAATGGCTCTCCTCAAGCGTATTCAACAAG   1619
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1588  GTTGTGAGTTGGATAGTTGTGGAAAGAGTCAAATGGCTCTCCTCAAGCGTATTCAACAAG   1647

Query   1620  GGGCTGAAGGATGCCCAGAAGGTACCCCATTGTATGGGATCTGATCTGGGGCCTCGGTGC   1679
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1648  GGGCTGAAGGATGCCCAGAAGGTACCCCATTGTATGGGATCTGATCTGGGGCCTCGGTGC   1707

Query   1680  ACATGCTTTACATGTGTTTAGTCGAGGTTaaaaaaaCGTCTAGGCCCCCCGAACCACGGG   1739
              |||||||||||||||||||||||||||||||       ||||||||||||||||||||||
Sbjct   1708  ACATGCTTTACATGTGTTTAGTCGAGGTTAAAAAA-CGTCTAGGCCCCCCGAACCACGGG   1766

Query   1740  GACGTGGTTTTCCTTTGAAAAACACGATGATACC    1773
              ||||||||||||||||||||||||||||| |||||
Sbjct   1767  GACGTGGTTTTCCTTTGAAAAACACGATAATACC    1800


>gb|FJ155667.1|  Allelic replacement vector pJC84, complete sequence
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Length=3775

Score = 1471 bits (796), Expect = 0.0
Identities = 796/796 (100%), Gaps = 0/796 (0%)
Strand=Plus/Minus

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Query  398   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   457
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2313  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   2254

Query  458   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   517
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2253  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   2194

Query  518   GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   577
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2193  GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   2134

Query  578   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   637
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2133  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   2074

Query  638   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   697
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2073  CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   2014

Query  698   GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   757
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2013  GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   1954

Query  758   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   817
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1953  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   1894

Query  818   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   877
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1893  ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   1834

Query  878   GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   937
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1833  GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   1774

Query  938   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   997
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1773  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   1714

Query  998   GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   1057
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1713  GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   1654

Query  1058  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   1117
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1653  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   1594

Query  1118  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   1177
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1593  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   1534

Query  1178  GACGAGTTCTTCTGAG    1193
             ||||||||||||||||
Sbjct  1533  GACGAGTTCTTCTGAG    1518
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>dbj|AB434475.1| Synthetic construct gfpuv5, aphA genes for green fluorescent
protein UV5, kanamycin resistance, complete cds, clone: pT2
Length=2773

Score = 1471 bits (796), Expect = 0.0
Identities = 796/796 (100%), Gaps = 0/796 (0%)
Strand=Plus/Plus

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Query  398   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   457
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1485  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   1544

Query  458   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   517
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1545  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   1604

Query  518   GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   577
```

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1605   GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   1664

Query   578   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG    637
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1665   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   1724

Query   638   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG    697
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1725   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   1784

Query   698   GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG    757
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1785   GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   1844

Query   758   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC    817
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1845   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   1904

Query   818   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA    877
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1905   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   1964

Query   878   GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC    937
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1965   GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   2024

Query   938   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT    997
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2025   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   2084

Query   998   GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   1057
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2085   GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   2144

Query  1058   ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   1117
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2145   ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   2204

Query  1118   CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   1177
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2205   CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   2264

Query  1178   GACGAGTTCTTCTGAG    1193
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Sbjct  2265   GACGAGTTCTTCTGAG    2280
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>dbj|AB434474.1| Synthetic construct gfpuv5, aphA genes for green fluorescent
protein UV5, kanamycin resistance, complete cds, clone: pT1
Length=3068

 Score = 1471 bits (796), Expect = 0.0
 Identities = 796/796 (100%), Gaps = 0/796 (0%)
 Strand=Plus/Plus

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Query   398   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC    457
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1780   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   1839

Query   458   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA    517
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1840   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   1899

Query   518   GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG    577
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1900   GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   1959

Query   578   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG    637
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1960   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   2019

Query   638   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG    697
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2020   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   2079

Query   698   GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG    757
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2080   GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   2139
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Query   758   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   817
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2140  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   2199

Query   818   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   877
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2200  ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   2259

Query   878   GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   937
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2260  GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   2319

Query   938   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   997
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2320  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   2379

Query   998   GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   1057
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2380  GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   2439

Query   1058  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   1117
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2440  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   2499

Query   1118  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   1177
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2500  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   2559

Query   1178  GACGAGTTCTTCTGAG      1193
              ||||||||||||||||
Sbjct   2560  GACGAGTTCTTCTGAG      2575
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>dbj|AB434472.1| Synthetic construct aphA, pyrE, gfpuv5 genes for kanamycin resi
orotate phosphoribosyltransferase, green fluorescent
protein UV5, complete cds, clone: OSU12-pyrE
Length=4263

Score = 1471 bits (796), Expect = 0.0
Identities = 796/796 (100%), Gaps = 0/796 (0%)
Strand=Plus/Minus

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Query   398   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   457
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1289  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   1230

Query   458   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   517
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1229  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   1170

Query   518   GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   577
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1169  GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   1110

Query   578   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   637
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1109  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   1050

Query   638   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   697
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1049  CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   990

Query   698   GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   757
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   989   GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   930

Query   758   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   817
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   929   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   870

Query   818   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   877
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   869   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   810

Query   878   GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   937
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   809   GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   750

Query   938   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   997
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Sbjct   749  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT  690

Query   998  GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC  1057
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   689  GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC  630

Query  1058  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC  1117
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   629  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC  570

Query  1118  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT  1177
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   569  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT  510

Query  1178  GACGAGTTCTTCTGAG     1193
             ||||||||||||||||
Sbjct   509  GACGAGTTCTTCTGAG     494
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>dbj|AB293446.1| ▨ Saccharomyces cerevisiae gene for aquaporin Aqy1, complete cd
clone: COS5
Length=45016

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 Score = 1471 bits (796),   Expect = 0.0
 Identities = 796/796 (100%), Gaps = 0/796 (0%)
 Strand=Plus/Plus

Query   398  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC  457
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 42231  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC  42290

Query   458  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA  517
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 42291  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA  42350

Query   518  GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG  577
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 42351  GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG  42410

Query   578  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG  637
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 42411  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG  42470

Query   638  CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG  697
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 42471  CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG  42530

Query   698  GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG  757
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 42531  GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG  42590

Query   758  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC  817
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 42591  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC  42650

Query   818  ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA  877
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 42651  ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA  42710

Query   878  GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC  937
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 42711  GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC  42770

Query   938  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT  997
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 42771  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT  42830

Query   998  GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC  1057
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 42831  GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC  42890

Query  1058  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC  1117
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 42891  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC  42950

Query  1118  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT  1177
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 42951  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT  43010
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Query  1178   GACGAGTTCTTCTGAG   1193
              |||||||||||||||||
Sbjct  43011  GACGAGTTCTTCTGAG   43026
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>dbj|AB293445.1| ▨ Saccharomyces cerevisiae gene for aquaporin Aqy1, complete cd
clone: COS4
Length=43682

 Score = 1471 bits (796), Expect = 0.0
 Identities = 796/796 (100%), Gaps = 0/796 (0%)
 Strand=Plus/Minus

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Query  398    ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   457
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4394   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   4335

Query  458    GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   517
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4334   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   4275

Query  518    GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   577
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4274   GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   4215

Query  578    CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   637
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4214   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   4155

Query  638    CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   697
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4154   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   4095

Query  698    GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   757
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4094   GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   4035

Query  758    CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   817
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4034   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   3975

Query  818    ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   877
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3974   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   3915

Query  878    GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   937
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3914   GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   3855

Query  938    GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   997
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3854   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   3795

Query  998    GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   1057
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3794   GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   3735

Query  1058   ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   1117
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3734   ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   3675

Query  1118   CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   1177
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3674   CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   3615

Query  1178   GACGAGTTCTTCTGAG   1193
              ||||||||||||||||
Sbjct  3614   GACGAGTTCTTCTGAG   3599
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>emb|FM162567.1| ▨ Trypanosoma brucei Lister 427 surface glycoprotein expression
site BES2/TAR129, from bloodstream
Length=51758

 Score = 1471 bits (796), Expect = 0.0
 Identities = 796/796 (100%), Gaps = 0/796 (0%)
 Strand=Plus/Plus

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Query   398   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   457
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1005  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   1064

Query   458   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   517
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1065  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   1124

Query   518   GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   577
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1125  GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   1184

Query   578   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   637
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1185  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   1244

Query   638   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   697
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1245  CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   1304

Query   698   GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   757
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1305  GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   1364

Query   758   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   817
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1365  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   1424

Query   818   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   877
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1425  ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   1484

Query   878   GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   937
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Sbjct   1485  GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   1544

Query   938   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   997
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1545  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   1604

Query   998   GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   1057
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Sbjct   1605  GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   1664

Query   1058  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   1117
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1665  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   1724

Query   1118  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   1177
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1725  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   1784

Query   1178  GACGAGTTCTTCTGAG     1193
              ||||||||||||||||
Sbjct   1785  GACGAGTTCTTCTGAG     1800
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>gb|EU491017.1| Suicide vector pEX18Km-pheS, complete sequence
Length=5161

 Score = 1471 bits (796), Expect = 0.0
 Identities = 796/796 (100%), Gaps = 0/796 (0%)
 Strand=Plus/Minus

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Query   398   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   457
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   4767  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   4708

Query   458   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   517
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   4707  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   4648

Query   518   GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   577
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   4647  GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   4588

Query   578   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   637
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   4587  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   4528
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Query  638   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   697
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Sbjct  4527  CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   4468

Query  698   GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   757
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4467  GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   4408

Query  758   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   817
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4407  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   4348

Query  818   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   877
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4347  ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   4288

Query  878   GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   937
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4287  GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   4228

Query  938   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   997
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4227  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   4168

Query  998   GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   1057
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Sbjct  4167  GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   4108

Query  1058  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   1117
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4107  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   4048

Query  1118  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   1177
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4047  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   3988

Query  1178  GACGAGTTCTTCTGAG    1193
             |||||||||||||||
Sbjct  3987  GACGAGTTCTTCTGAG    3972
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>gb|EU232662.1| Cloning vector pVMGCRT85, complete sequence
Length=11368

 Score = 1471 bits (796), Expect = 0.0
 Identities = 796/796 (100%), Gaps = 0/796 (0%)
 Strand=Plus/Plus

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Query  398   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   457
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3541  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   3600

Query  458   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   517
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3601  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   3660

Query  518   GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   577
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3661  GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   3720

Query  578   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   637
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3721  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   3780

Query  638   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   697
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3781  CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   3840

Query  698   GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   757
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3841  GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   3900

Query  758   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   817
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3901  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   3960

Query  818   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   877
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3961  ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   4020
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Query   878   GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   937
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   4021  GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   4080

Query   938   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   997
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   4081  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   4140

Query   998   GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   1057
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   4141  GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   4200

Query   1058  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   1117
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   4201  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   4260

Query   1118  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   1177
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   4261  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   4320

Query   1178  GACGAGTTCTTCTGAG      1193
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Sbjct   4321  GACGAGTTCTTCTGAG      4336


>gb|EU232661.1|  Cloning vector pVMG-TnpR, complete sequence
Length=7264

 Score = 1471 bits (796),  Expect = 0.0
 Identities = 796/796 (100%), Gaps = 0/796 (0%)
 Strand=Plus/Plus

Query   398   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   457
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3019  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   3078

Query   458   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   517
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3079  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   3138

Query   518   GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   577
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3139  GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   3198

Query   578   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   637
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3199  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   3258

Query   638   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   697
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3259  CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   3318

Query   698   GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   757
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3319  GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   3378

Query   758   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   817
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3379  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   3438

Query   818   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   877
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3439  ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   3498

Query   878   GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   937
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3499  GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   3558

Query   938   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   997
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3559  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   3618

Query   998   GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   1057
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3619  GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   3678

Query   1058  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   1117
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3679  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   3738
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Query  1118  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT  1177
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3739  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT  3798

Query  1178  GACGAGTTCTTCTGAG   1193
             ||||||||||||||||
Sbjct  3799  GACGAGTTCTTCTGAG   3814
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>dbj|AB366441.1| ▨ Salmonella enterica subsp. enterica serovar Dublin plasmid pM
DNA, complete genome, strain: L-789
Length=61571

 Score = 1471 bits (796), Expect = 0.0
 Identities = 796/796 (100%), Gaps = 0/796 (0%)
 Strand=Plus/Plus

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Query  398    ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC  457
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Sbjct  10076  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC  10135

Query  458    GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA  517
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  10136  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA  10195

Query  518    GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG  577
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  10196  GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG  10255

Query  578    CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG  637
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  10256  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG  10315

Query  638    CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG  697
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  10316  CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG  10375

Query  698    GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG  757
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  10376  GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG  10435

Query  758    CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC  817
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  10436  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC  10495

Query  818    ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA  877
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  10496  ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA  10555

Query  878    GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC  937
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  10556  GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC  10615

Query  938    GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT  997
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  10616  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT  10675

Query  998    GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC  1057
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  10676  GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC  10735

Query  1058   ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC  1117
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  10736  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC  10795

Query  1118   CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT  1177
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  10796  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT  10855

Query  1178   GACGAGTTCTTCTGAG   1193
              ||||||||||||||||
Sbjct  10856  GACGAGTTCTTCTGAG   10871
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>gb|EU047752.1| ▨ Cloning vector pDC8, complete sequence
Length=11987

Sort alignments for this
E value Score Percen
Query start position

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Score = 1471 bits (796),  Expect = 0.0
Identities = 796/796 (100%), Gaps = 0/796 (0%)
Strand=Plus/Plus

Query  398   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC  457
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  7100  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC  7159

Query  458   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA  517
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  7160  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA  7219

Query  518   GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG  577
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  7220  GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG  7279

Query  578   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG  637
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  7280  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG  7339

Query  638   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG  697
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  7340  CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG  7399

Query  698   GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG  757
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  7400  GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG  7459

Query  758   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC  817
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  7460  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC  7519

Query  818   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA  877
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  7520  ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA  7579

Query  878   GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC  937
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  7580  GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC  7639

Query  938   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT  997
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  7640  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT  7699

Query  998   GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC  1057
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  7700  GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC  7759

Query  1058  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC  1117
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  7760  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC  7819

Query  1118  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT  1177
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  7820  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT  7879

Query  1178  GACGAGTTCTTCTGAG      1193
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Sbjct  7880  GACGAGTTCTTCTGAG      7895


Score =  706 bits (382),  Expect = 0.0
Identities = 382/382 (100%), Gaps = 0/382 (0%)
Strand=Plus/Minus

Query  398    ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC  457
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  11249  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC  11190

Query  458    GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA  517
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  11189  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA  11130

Query  518    GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG  577
              |||||||||||||||||||||||||||||||||||||||||||||||||| || ||||||||
Sbjct  11129  GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG  11070
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Query   578    CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG    637
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   11069  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG    11010

Query   638    CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG    697
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   11009  CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG    10950

Query   698    GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG    757
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   10949  GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG    10890

Query   758    CGGCGGCTGCATACGCTTGATC        779
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>gb|EU024548.1|  Cloning vector pCPP5250, complete sequence
Length=5155

 Score = 1471 bits (796),  Expect = 0.0
 Identities = 796/796 (100%), Gaps = 0/796 (0%)
 Strand=Plus/Plus

Query   398    ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC    457
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Sbjct   2347   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC    2406

Query   458    GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA    517
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2407   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA    2466

Query   518    GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG    577
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2467   GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG    2526

Query   578    CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG    637
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2527   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG    2586

Query   638    CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG    697
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2587   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG    2646

Query   698    GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG    757
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Sbjct   2647   GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG    2706

Query   758    CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC    817
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2707   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC    2766

Query   818    ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA    877
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2767   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA    2826

Query   878    GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC    937
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2827   GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC    2886

Query   938    GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT    997
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2887   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT    2946

Query   998    GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC    1057
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Sbjct   2947   GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC    3006

Query   1058   ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC    1117
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3007   ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC    3066

Query   1118   CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT    1177
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Sbjct   3067   CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT    3126

Query   1178   GACGAGTTCTTCTGAG        1193
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Sbjct   3127   GACGAGTTCTTCTGAG        3142
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>gb|EU024546.1|  Cloning vector pCPP5702, complete sequence
Length=8791

 Score = 1471 bits (796),  Expect = 0.0
 Identities = 796/796 (100%), Gaps = 0/796 (0%)
 Strand=Plus/Minus

Query  398   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC  457
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Sbjct  2827  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC  2768

Query  458   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA  517
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2767  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA  2708

Query  518   GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG  577
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2707  GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG  2648

Query  578   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG  637
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2647  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG  2588

Query  638   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG  697
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2587  CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG  2528

Query  698   GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG  757
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2527  GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG  2468

Query  758   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC  817
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2467  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC  2408

Query  818   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA  877
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2407  ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA  2348

Query  878   GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC  937
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2347  GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC  2288

Query  938   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT  997
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2287  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT  2228

Query  998   GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC  1057
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2227  GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC  2168

Query  1058  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC  1117
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2167  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC  2108

Query  1118  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT  1177
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2107  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT  2048

Query  1178  GACGAGTTCTTCTGAG    1193
             ||||||||||||||||
Sbjct  2047  GACGAGTTCTTCTGAG    2032


>gb|EF437956.1|  Expression vector pcDNA3-AQP4f, complete sequence
Length=6510

 Score = 1471 bits (796),  Expect = 0.0
 Identities = 796/796 (100%), Gaps = 0/796 (0%)
 Strand=Plus/Plus

Query  398   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC  457
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3215  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC  3274

Query  458   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA  517
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3275  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA  3334
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Query   518   GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   577
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3335  GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   3394

Query   578   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   637
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3395  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   3454

Query   638   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   697
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3455  CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   3514

Query   698   GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   757
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3515  GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   3574

Query   758   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   817
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3575  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   3634

Query   818   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   877
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3635  ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   3694

Query   878   GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   937
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3695  GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   3754

Query   938   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   997
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3755  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   3814

Query   998   GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   1057
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3815  GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   3874

Query   1058  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   1117
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3875  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   3934

Query   1118  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   1177
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3935  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   3994

Query   1178  GACGAGTTCTTCTGAG      1193
              ||||||||||||||||
Sbjct   3995  GACGAGTTCTTCTGAG      4010
```

>gb|EF437953.1| Expression vector pcDNA3-AQP4e, complete sequence
Length=6675

 Score = 1471 bits (796), Expect = 0.0
 Identities = 796/796 (100%), Gaps = 0/796 (0%)
 Strand=Plus/Plus

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Query   398   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   457
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3380  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   3439

Query   458   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   517
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3440  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   3499

Query   518   GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   577
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3500  GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   3559

Query   578   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   637
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3560  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   3619

Query   638   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   697
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3620  CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   3679

Query   698   GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   757
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3680  GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   3739
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Query   758   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   817
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3740  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   3799

Query   818   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   877
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3800  ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   3859

Query   878   GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   937
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3860  GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   3919

Query   938   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   997
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3920  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   3979

Query   998   GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   1057
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3980  GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   4039

Query   1058  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   1117
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   4040  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   4099

Query   1118  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   1177
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   4100  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   4159

Query   1178  GACGAGTTCTTCTGAG      1193
              ||||||||||||||||
Sbjct   4160  GACGAGTTCTTCTGAG      4175
```

>gb|EF437951.1| Expression vector pcDNA3-AQP4d, complete sequence
Length=6349

 Score = 1471 bits (796), Expect = 0.0
 Identities = 796/796 (100%), Gaps = 0/796 (0%)
 Strand=Plus/Plus

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Query   398   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   457
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3054  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   3113

Query   458   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   517
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3114  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   3173

Query   518   GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   577
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3174  GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   3233

Query   578   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   637
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3234  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   3293

Query   638   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   697
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3294  CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   3353

Query   698   GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   757
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3354  GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   3413

Query   758   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   817
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3414  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   3473

Query   818   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   877
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3474  ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   3533

Query   878   GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   937
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3534  GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   3593

Query   938   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   997
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3594  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   3653
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```
Query   998   GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   1057
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3654  GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   3713

Query   1058  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   1117
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3714  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   3773

Query   1118  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   1177
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3774  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   3833

Query   1178  GACGAGTTCTTCTGAG   1193
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Sbjct   3834  GACGAGTTCTTCTGAG   3849


>gb|EF437950.1|  Expression vector pcDNA3-K-AQP4d, complete sequence
Length=6161

 Score = 1471 bits (796),  Expect = 0.0
 Identities = 796/796 (100%), Gaps = 0/796 (0%)
 Strand=Plus/Plus

Query   398   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   457
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2866  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   2925

Query   458   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   517
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2926  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   2985

Query   518   GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   577
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2986  GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   3045

Query   578   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   637
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3046  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   3105

Query   638   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   697
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3106  CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   3165

Query   698   GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   757
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3166  GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   3225

Query   758   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   817
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3226  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   3285

Query   818   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   877
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3286  ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   3345

Query   878   GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   937
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3346  GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   3405

Query   938   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   997
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3406  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   3465

Query   998   GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   1057
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3466  GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   3525

Query   1058  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   1117
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3526  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   3585

Query   1118  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   1177
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3586  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   3645

Query   1178  GACGAGTTCTTCTGAG   1193
              ||||||||||||||||
Sbjct   3646  GACGAGTTCTTCTGAG   3661
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>gb|CP000744.1| 🔲 Pseudomonas aeruginosa PA7, complete genome
Length=6588339

 Features in this part of subject sequence:
   aminoglycoside 3'-phosphotransferase

 Score = 1471 bits (796), Expect = 0.0
 Identities = 796/796 (100%), Gaps = 0/796 (0%)
 Strand=Plus/Minus

```
Query  398    ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC  457
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3858355 ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC  385

Query  458    GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA  517
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3858295 GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA  385

Query  518    GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG  577
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3858235 GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG  385

Query  578    CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG  637
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3858175 CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG  385

Query  638    CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG  697
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3858115 CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG  385

Query  698    GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG  757
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3858055 GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG  385

Query  758    CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC  817
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3857995 CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC  385

Query  818    ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA  877
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3857935 ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA  385

Query  878    GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC  937
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3857875 GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC  385

Query  938    GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT  997
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3857815 GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT  385

Query  998    GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC  105
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3857755 GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC  385

Query  1058   ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC  111
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3857695 ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC  385

Query  1118   CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT  117
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3857635 CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT  385

Query  1178   GACGAGTTCTTCTGAG    1193
              ||||||||||||||||
Sbjct  3857575 GACGAGTTCTTCTGAG    3857560
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>gb|AY667410.1| 🔲 Shuttle cosmid vector pHZ1358, complete sequence
Length=10848

 Score = 1471 bits (796), Expect = 0.0
 Identities = 796/796 (100%), Gaps = 0/796 (0%)
 Strand=Plus/Minus

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Query  398    ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC  457
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Sbjct  4245  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC  4186

Query   458  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA  517
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4185  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA  4126

Query   518  GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG  577
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4125  GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG  4066

Query   578  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG  637
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4065  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG  4006

Query   638  CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG  697
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4005  CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG  3946

Query   698  GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG  757
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3945  GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG  3886

Query   758  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC  817
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3885  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC  3826

Query   818  ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA  877
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3825  ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA  3766

Query   878  GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC  937
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3765  GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC  3706

Query   938  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT  997
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3705  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT  3646

Query   998  GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC  1057
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3645  GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC  3586

Query  1058  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC  1117
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3585  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC  3526

Query  1118  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT  1177
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3525  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT  3466

Query  1178  GACGAGTTCTTCTGAG    1193
             ||||||||||||||||
Sbjct  3465  GACGAGTTCTTCTGAG    3450
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>emb|AM711972.1| Transposon mutagenesis vector pMiET
Length=7819

 Score = 1471 bits (796),   Expect = 0.0
 Identities = 796/796 (100%), Gaps = 0/796 (0%)
 Strand=Plus/Plus

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Query   398  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC  457
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  6494  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC  6553

Query   458  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA  517
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  6554  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA  6613

Query   518  GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG  577
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  6614  GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG  6673

Query   578  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG  637
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  6674  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG  6733

Query   638  CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG  697
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Sbjct   6734   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   6793

Query    698   GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG    757
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   6794   GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   6853

Query    758   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC    817
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   6854   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   6913

Query    818   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA    877
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   6914   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   6973

Query    878   GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC    937
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   6974   GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   7033

Query    938   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT    997
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   7034   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   7093

Query    998   GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   1057
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   7094   GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   7153

Query   1058   ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   1117
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   7154   ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   7213

Query   1118   CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   1177
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   7214   CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   7273

Query   1178   GACGAGTTCTTCTGAG       1193
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Sbjct   7274   GACGAGTTCTTCTGAG       7289


>gb|EF550208.1|  Cloning vector pcDNA3.1+PA, complete sequence
Length=7063

 Score = 1471 bits (796),  Expect = 0.0
 Identities = 796/796 (100%), Gaps = 0/796 (0%)
 Strand=Plus/Plus

Query    398   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC    457
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Sbjct   3771   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   3830

Query    458   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA    517
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3831   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   3890

Query    518   GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG    577
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3891   GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   3950

Query    578   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG    637
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3951   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   4010

Query    638   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG    697
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   4011   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   4070

Query    698   GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG    757
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   4071   GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   4130

Query    758   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC    817
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   4131   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   4190

Query    818   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA    877
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   4191   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   4250

Query    878   GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC    937
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Sbjct  4251  GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC  4310

Query  938   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT  997
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4311  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT  4370

Query  998   GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC  1057
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4371  GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC  4430

Query  1058  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC  1117
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4431  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC  4490

Query  1118  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT  1177
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4491  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT  4550

Query  1178  GACGAGTTCTTCTGAG  1193
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Sbjct  4551  GACGAGTTCTTCTGAG  4566


>gb|EF192606.1|      Cloning vector pBEO210, complete sequence
Length=28953

 Score = 1471 bits (796),  Expect = 0.0
 Identities = 796/796 (100%), Gaps = 0/796 (0%)
 Strand=Plus/Plus

Query  398    ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC  457
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  16387  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC  16446

Query  458    GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA  517
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  16447  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA  16506

Query  518    GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG  577
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  16507  GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG  16566

Query  578    CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG  637
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  16567  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG  16626

Query  638    CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG  697
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  16627  CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG  16686

Query  698    GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG  757
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  16687  GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG  16746

Query  758    CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC  817
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  16747  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC  16806

Query  818    ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA  877
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  16807  ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA  16866

Query  878    GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC  937
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  16867  GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC  16926

Query  938    GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT  997
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  16927  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT  16986

Query  998    GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC  1057
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  16987  GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC  17046

Query  1058   ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC  1117
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  17047  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC  17106

Query  1118   CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT  1177
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Sbjct  17107  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT  17166

Query   1178  GACGAGTTCTTCTGAG    1193
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Sbjct  17167  GACGAGTTCTTCTGAG  17182
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>gb|EF028675.1| Cloning vector pDV-NTAP-CYFP, complete sequence
Length=8003

 Score = 1471 bits (796), Expect = 0.0
 Identities = 796/796 (100%), Gaps = 0/796 (0%)
 Strand=Plus/Plus

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Query    398  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC  457
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3062  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC  3121

Query    458  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA  517
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3122  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA  3181

Query    518  GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG  577
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3182  GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG  3241

Query    578  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG  637
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3242  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG  3301

Query    638  CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG  697
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3302  CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG  3361

Query    698  GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG  757
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3362  GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG  3421

Query    758  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC  817
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3422  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC  3481

Query    818  ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA  877
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3482  ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA  3541

Query    878  GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC  937
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3542  GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC  3601

Query    938  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT  997
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3602  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT  3661

Query    998  GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC  1057
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3662  GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC  3721

Query   1058  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC  1117
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Sbjct   3722  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC  3781

Query   1118  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT  1177
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Sbjct   3782  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT  3841

Query   1178  GACGAGTTCTTCTGAG    1193
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Sbjct   3842  GACGAGTTCTTCTGAG  3857
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>gb|EF028674.1| Cloning vector pDV-NTAP-CGFP, complete sequence
Length=8003

 Score = 1471 bits (796), Expect = 0.0
 Identities = 796/796 (100%), Gaps = 0/796 (0%)
 Strand=Plus/Plus

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Query    398  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC  457
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Sbjct  3062  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC  3121

Query  458   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA  517
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3122  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA  3181

Query  518   GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG  577
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3182  GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG  3241

Query  578   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG  637
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3242  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG  3301

Query  638   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG  697
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Sbjct  3302  CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG  3361

Query  698   GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG  757
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3362  GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG  3421

Query  758   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC  817
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Sbjct  3422  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC  3481

Query  818   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA  877
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Sbjct  3482  ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA  3541

Query  878   GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC  937
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Sbjct  3542  GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC  3601

Query  938   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT  997
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Sbjct  3602  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT  3661

Query  998   GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC  1057
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Sbjct  3662  GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC  3721

Query  1058  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC  1117
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Sbjct  3722  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC  3781

Query  1118  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT  1177
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3782  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT  3841

Query  1178  GACGAGTTCTTCTGAG     1193
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Sbjct  3842  GACGAGTTCTTCTGAG     3857
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>gb|EF028673.1| Cloning vector pDV-CYFP-CTAP, complete sequence
Length=8021

 Score = 1471 bits (796), Expect = 0.0
 Identities = 796/796 (100%), Gaps = 0/796 (0%)
 Strand=Plus/Plus

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Query  398   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC  457
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Sbjct  3080  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC  3139

Query  458   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA  517
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Sbjct  3140  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA  3199

Query  518   GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG  577
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Sbjct  3200  GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG  3259

Query  578   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG  637
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Sbjct  3260  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG  3319

Query  638   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG  697
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Sbjct  3320  CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG  3379

Query   698  GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   757
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Sbjct  3380  GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG  3439

Query   758  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   817
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Sbjct  3440  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC  3499

Query   818  ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   877
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Sbjct  3500  ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA  3559

Query   878  GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   937
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Sbjct  3560  GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC  3619

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Sbjct  3620  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT  3679

Query   998  GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC  1057
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Sbjct  3680  GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC  3739

Query  1058  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC  1117
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Sbjct  3740  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC  3799

Query  1118  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT  1177
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Sbjct  3800  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT  3859

Query  1178  GACGAGTTCTTCTGAG     1193
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Sbjct  3860  GACGAGTTCTTCTGAG     3875
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>gb|EF028672.1| Cloning vector pDV-CGFP-CTAP, complete sequence
Length=8021

 Score = 1471 bits (796), Expect = 0.0
 Identities = 796/796 (100%), Gaps = 0/796 (0%)
 Strand=Plus/Plus

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Query   398  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   457
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Sbjct  3080  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC  3139

Query   458  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   517
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Sbjct  3140  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA  3199

Query   518  GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   577
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Sbjct  3200  GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG  3259

Query   578  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   637
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3260  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG  3319

Query   638  CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   697
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Query   698  GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   757
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3380  GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG  3439

Query   758  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   817
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Sbjct  3440  CGGCGgCTGCATACGCTTGATcCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC  3499

Query   818  ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   877
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Sbjct  3500  ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA  3559

Query   878  GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   937
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Sbjct  3560  GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC  3619

Query   938  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT  997
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Sbjct  3620  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT  3679

Query   998  GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC  1057
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Sbjct  3680  GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC  3739

Query  1058  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC  1117
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Sbjct  3740  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC  3799

Query  1118  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT  1177
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Sbjct  3800  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT  3859

Query  1178  GACGAGTTCTTCTGAG      1193
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Sbjct  3860  GACGAGTTCTTCTGAG      3875
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>gb|EF028671.1| Cloning vector pDV-NYFP-CTAP, complete sequence
Length=8021

 Score = 1471 bits (796), Expect = 0.0
 Identities = 796/796 (100%), Gaps = 0/796 (0%)
 Strand=Plus/Plus

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Query   398  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC  457
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Sbjct  3080  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC  3139

Query   458  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA  517
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Sbjct  3140  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA  3199

Query   518  GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG  577
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Sbjct  3200  GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG  3259

Query   578  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG  637
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Sbjct  3260  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG  3319

Query   638  CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG  697
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Sbjct  3320  CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG  3379

Query   698  GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG  757
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Sbjct  3380  GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG  3439

Query   758  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC  817
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Sbjct  3440  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC  3499

Query   818  ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA  877
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Query   878  GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC  937
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Sbjct  3620  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT  3679

Query   998  GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC  1057
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Sbjct  3680  GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC  3739

Query  1058  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC  1117
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Sbjct  3740  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC  3799

Query  1118  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT  1177
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Sbjct  3800  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT  3859

Query  1178  GACGAGTTCTTCTGAG    1193
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Sbjct  3860  GACGAGTTCTTCTGAG    3875
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>gb|EF028670.1| Cloning vector pDV-NTAP-NYFP, complete sequence
Length=8003

 Score = 1471 bits (796), Expect = 0.0
 Identities = 796/796 (100%), Gaps = 0/796 (0%)
 Strand=Plus/Plus

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Query   398  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   457
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3062  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC  3121

Query   458  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   517
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3122  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA  3181

Query   518  GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   577
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3182  GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG  3241

Query   578  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   637
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Sbjct  3242  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG  3301

Query   638  CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   697
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Sbjct  3302  CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG  3361

Query   698  GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   757
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Sbjct  3362  GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG  3421

Query   758  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   817
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Sbjct  3422  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC  3481

Query   818  ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   877
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Sbjct  3482  ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA  3541

Query   878  GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   937
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Sbjct  3542  GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC  3601

Query   938  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   997
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Sbjct  3602  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT  3661

Query   998  GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC  1057
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Sbjct  3662  GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC  3721

Query  1058  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC  1117
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Sbjct  3722  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC  3781

Query  1118  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT  1177
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Sbjct  3782  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT  3841

Query  1178  GACGAGTTCTTCTGAG    1193
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>gb|EF028669.1| Cloning vector pDV-CTAP, complete sequence
Length=7307

 Score = 1471 bits (796), Expect = 0.0
 Identities = 796/796 (100%), Gaps = 0/796 (0%)
 Strand=Plus/Plus

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Query   398  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   457
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Sbjct  2366   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   2425

Query   458   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   517
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2426   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   2485

Query   518   GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   577
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2486   GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   2545

Query   578   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   637
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2546   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   2605

Query   638   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   697
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2606   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   2665

Query   698   GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   757
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2666   GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   2725

Query   758   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   817
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2726   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   2785

Query   818   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   877
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2786   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   2845

Query   878   GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   937
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2846   GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   2905

Query   938   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   997
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2906   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   2965

Query   998   GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   1057
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2966   GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   3025

Query  1058   ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   1117
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3026   ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   3085

Query  1118   CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   1177
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3086   CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   3145

Query  1178   GACGAGTTCTTCTGAG    1193
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Sbjct  3146   GACGAGTTCTTCTGAG    3161
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>gb|EF028668.1| Cloning vector pDV-CYFP, complete sequence
Length=7475

 Score = 1471 bits (796), Expect = 0.0
 Identities = 796/796 (100%), Gaps = 0/796 (0%)
 Strand=Plus/Plus

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Query   398   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   457
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2534   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   2593

Query   458   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   517
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2594   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   2653

Query   518   GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   577
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2654   GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   2713

Query   578   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   637
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2714   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   2773

Query   638   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   697
```

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                     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2774   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   2833

Query    698   GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   757
                     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2834   GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   2893

Query    758   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   817
                     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2894   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   2953

Query    818   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   877
                     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2954   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   3013

Query    878   GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   937
                     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3014   GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   3073

Query    938   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   997
                     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3074   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   3133

Query    998   GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   1057
                     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3134   GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   3193

Query   1058   ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   1117
                     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3194   ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   3253

Query   1118   CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   1177
                     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3254   CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   3313

Query   1178   GACGAGTTCTTCTGAG     1193
                     ||||||||||||||||
Sbjct   3314   GACGAGTTCTTCTGAG     3329
```

>gb|EF028667.1| Cloning vector pDV-CGFP, complete sequence
Length=7475

 Score = 1471 bits (796), Expect = 0.0
 Identities = 796/796 (100%), Gaps = 0/796 (0%)
 Strand=Plus/Plus

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Query    398   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   457
                     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2534   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   2593

Query    458   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   517
                     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2594   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   2653

Query    518   GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   577
                     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2654   GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   2713

Query    578   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   637
                     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2714   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   2773

Query    638   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   697
                     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2774   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   2833

Query    698   GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   757
                     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2834   GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   2893

Query    758   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   817
                     ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Sbjct   2894   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   2953

Query    818   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   877
                     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2954   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   3013

Query    878   GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   937
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Sbjct  3014  GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC  3073

Query   938  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT  997
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3074  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT  3133

Query   998  GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC  1057
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3134  GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC  3193

Query  1058  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC  1117
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3194  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC  3253

Query  1118  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT  1177
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3254  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT  3313

Query  1178  GACGAGTTCTTCTGAG      1193
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Sbjct  3314  GACGAGTTCTTCTGAG      3329
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>gb|EF028666.1| Cloning vector pDV-NTAP, complete sequence
Length=7289

 Score = 1471 bits (796), Expect = 0.0
 Identities = 796/796 (100%), Gaps = 0/796 (0%)
 Strand=Plus/Plus

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Query   398  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC  457
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2348  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC  2407

Query   458  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA  517
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2408  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA  2467

Query   518  GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG  577
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2468  GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG  2527

Query   578  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG  637
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2528  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG  2587

Query   638  CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG  697
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2588  CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG  2647

Query   698  GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG  757
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2648  GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG  2707

Query   758  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC  817
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2708  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC  2767

Query   818  ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA  877
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2768  ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA  2827

Query   878  GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC  937
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2828  GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC  2887

Query   938  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT  997
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2888  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT  2947

Query   998  GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC  1057
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2948  GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC  3007

Query  1058  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC  1117
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3008  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC  3067

Query  1118  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT  1177
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3068   CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT  3127

Query  1178   GACGAGTTCTTCTGAG    1193
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Sbjct  3128   GACGAGTTCTTCTGAG    3143
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>gb|EF028665.1| Cloning vector pDV-NYFP, complete sequence
Length=7475

 Score = 1471 bits (796), Expect = 0.0
 Identities = 796/796 (100%), Gaps = 0/796 (0%)
 Strand=Plus/Plus

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Query  398    ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC  457
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2534   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC  2593

Query  458    GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA  517
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2594   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA  2653

Query  518    GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG  577
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2654   GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG  2713

Query  578    CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG  637
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2714   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG  2773

Query  638    CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG  697
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2774   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG  2833

Query  698    GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG  757
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2834   GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG  2893

Query  758    CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC  817
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2894   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC  2953

Query  818    ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA  877
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2954   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA  3013

Query  878    GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC  937
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3014   GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC  3073

Query  938    GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT  997
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3074   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT  3133

Query  998    GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC  1057
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3134   GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC  3193

Query  1058   ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC  1117
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3194   ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC  3253

Query  1118   CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT  1177
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3254   CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT  3313

Query  1178   GACGAGTTCTTCTGAG    1193
              ||||||||||||||||
Sbjct  3314   GACGAGTTCTTCTGAG    3329
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>gb|EF028664.1| Cloning vector EXP5(+), complete sequence
Length=6761

 Score = 1471 bits (796), Expect = 0.0
 Identities = 796/796 (100%), Gaps = 0/796 (0%)
 Strand=Plus/Plus

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Query  398    ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC  457
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Sbjct  1820  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC  1879

Query   458  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   517
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1880  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA  1939

Query   518  GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   577
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1940  GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG  1999

Query   578  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   637
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2000  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG  2059

Query   638  CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   697
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2060  CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG  2119

Query   698  GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   757
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2120  GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG  2179

Query   758  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   817
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2180  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC  2239

Query   818  ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   877
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2240  ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA  2299

Query   878  GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   937
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2300  GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC  2359

Query   938  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   997
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2360  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT  2419

Query   998  GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC  1057
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2420  GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC  2479

Query  1058  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC  1117
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2480  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC  2539

Query  1118  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT  1177
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2540  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT  2599

Query  1178  GACGAGTTCTTCTGAG    1193
                ||||||||||||||||
Sbjct  2600  GACGAGTTCTTCTGAG    2615
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>gb|EF028663.1| Cloning vector EXP4(+), complete sequence
Length=6724

 Score = 1471 bits (796), Expect = 0.0
 Identities = 796/796 (100%), Gaps = 0/796 (0%)
 Strand=Plus/Plus

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Query   398  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   457
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1791  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC  1850

Query   458  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   517
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1851  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA  1910

Query   518  GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   577
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1911  GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG  1970

Query   578  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   637
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1971  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG  2030

Query   638  CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   697
```

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              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2031   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   2090

Query  698    GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   757
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2091   GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   2150

Query  758    CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   817
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2151   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   2210

Query  818    ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   877
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2211   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   2270

Query  878    GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   937
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2271   GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   2330

Query  938    GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   997
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2331   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   2390

Query  998    GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   1057
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2391   GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   2450

Query  1058   ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   1117
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2451   ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   2510

Query  1118   CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   1177
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2511   CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   2570

Query  1178   GACGAGTTCTTCTGAG     1193
              ||||||||||||||||
Sbjct  2571   GACGAGTTCTTCTGAG     2586
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>gb|EF177812.1| Expression vector pUNIV, complete sequence
Length=5653

 Score = 1471 bits (796), Expect = 0.0
 Identities = 796/796 (100%), Gaps = 0/796 (0%)
 Strand=Plus/Plus

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Query  398    ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   457
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2644   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   2703

Query  458    GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   517
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2704   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   2763

Query  518    GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   577
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2764   GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   2823

Query  578    CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   637
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2824   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   2883

Query  638    CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   697
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2884   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   2943

Query  698    GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   757
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2944   GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   3003

Query  758    CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   817
              |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3004   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   3063

Query  818    ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   877
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3064   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   3123

Query  878    GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   937
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3124   GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   3183

Query  938    GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   997
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3184   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   3243

Query  998    GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   1057
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3244   GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   3303

Query  1058   ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   1117
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3304   ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   3363

Query  1118   CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   1177
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3364   CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   3423

Query  1178   GACGAGTTCTTCTGAG   1193
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Sbjct  3424   GACGAGTTCTTCTGAG   3439
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>gb|EF030522.1| Inducible protein expression vector pReg Neo, complete sequence
Length=6802

 Score = 1471 bits (796), Expect = 0.0
 Identities = 796/796 (100%), Gaps = 0/796 (0%)
 Strand=Plus/Plus

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Query  398    ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   457
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Sbjct  3793   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   3852

Query  458    GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   517
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3853   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   3912

Query  518    GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   577
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3913   GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   3972

Query  578    CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   637
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3973   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   4032

Query  638    CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   697
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4033   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   4092

Query  698    GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   757
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4093   GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   4152

Query  758    CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   817
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4153   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   4212

Query  818    ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   877
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4213   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   4272

Query  878    GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   937
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4273   GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   4332

Query  938    GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   997
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4333   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   4392

Query  998    GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   1057
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4393   GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   4452

Query  1058   ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   1117
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4453   ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   4512

Query  1118   CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   1177
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Sbjct  4513  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT  4572

Query  1178  GACGAGTTCTTCTGAG   1193
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Sbjct  4573  GACGAGTTCTTCTGAG   4588
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>dbj|AB255435.1| ▓ Escherichia coli plasmid pO86A1 DNA, complete sequence
Length=120730

 Score = 1471 bits (796), Expect = 0.0
 Identities = 796/796 (100%), Gaps = 0/796 (0%)
 Strand=Plus/Plus

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Query   398    ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   457
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Sbjct  116462  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   1165

Query   458    GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   517
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  116522  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   1165

Query   518    GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   577
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  116582  GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   1166

Query   578    CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   637
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  116642  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   1167

Query   638    CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   697
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  116702  CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   1167

Query   698    GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   757
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Sbjct  116762  GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   1168

Query   758    CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   817
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  116822  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   1168

Query   818    ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   877
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  116882  ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   1169

Query   878    GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   937
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Sbjct  116942  GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   1170

Query   938    GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   997
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  117002  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   1170

Query   998    GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   1057
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Sbjct  117062  GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   1171

Query  1058    ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   1117
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  117122  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   1171

Query  1118    CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   1177
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Sbjct  117182  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   1172

Query  1178    GACGAGTTCTTCTGAG   1193
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Sbjct  117242  GACGAGTTCTTCTGAG   117257
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>gb|DQ886588.1| Expression vector pcDNA3-hFIX, complete sequence
Length=8223

 Score = 1471 bits (796), Expect = 0.0
 Identities = 796/796 (100%), Gaps = 0/796 (0%)
 Strand=Plus/Plus

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Query   398   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   457
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   4928  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   4987

Query   458   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   517
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   4988  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   5047

Query   518   GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   577
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   5048  GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   5107

Query   578   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   637
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   5108  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   5167

Query   638   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   697
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   5168  CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   5227

Query   698   GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   757
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   5228  GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   5287

Query   758   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   817
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   5288  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   5347

Query   818   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   877
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   5348  ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   5407

Query   878   GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   937
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   5408  GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   5467

Query   938   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   997
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   5468  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   5527

Query   998   GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   1057
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   5528  GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   5587

Query   1058  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   1117
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   5588  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   5647

Query   1118  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   1177
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   5648  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   5707

Query   1178  GACGAGTTCTTCTGAG      1193
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Sbjct   5708  GACGAGTTCTTCTGAG      5723


>gb|DQ898181.1|  Keratinocyte expression vector phPK14H, complete sequence
Length=6815

 Score = 1471 bits (796),  Expect = 0.0
 Identities = 796/796 (100%), Gaps = 0/796 (0%)
 Strand=Plus/Plus

Query   398   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   457
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3520  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   3579

Query   458   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   517
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3580  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   3639

Query   518   GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   577
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3640  GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   3699

Query   578   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   637
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3700  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   3759
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Query  638   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   697
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3760  CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   3819

Query  698   GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   757
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3820  GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   3879

Query  758   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   817
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3880  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   3939

Query  818   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   877
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3940  ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   3999

Query  878   GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   937
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4000  GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   4059

Query  938   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   997
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4060  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   4119

Query  998   GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   1057
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4120  GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   4179

Query  1058  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   1117
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4180  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   4239

Query  1118  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   1177
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4240  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   4299

Query  1178  GACGAGTTCTTCTGAG    1193
             ||||||||||||||||
Sbjct  4300  GACGAGTTCTTCTGAG    4315
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>gb|DQ823233.1| 🔲 Expression vector mce4, complete sequence
Length=29048

 Score = 1471 bits (796), Expect = 0.0
 Identities = 796/796 (100%), Gaps = 0/796 (0%)
 Strand=Plus/Plus

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Query  398    ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   457
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  25966  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   26025

Query  458    GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   517
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  26026  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   26085

Query  518    GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   577
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  26086  GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   26145

Query  578    CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   637
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  26146  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   26205

Query  638    CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   697
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  26206  CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   26265

Query  698    GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   757
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  26266  GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   26325

Query  758    CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   817
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  26326  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   26385

Query  818    ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   877
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  26386  ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   26445
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Query   878    GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   937
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   26446  GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   26505

Query   938    GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   997
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   26506  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   26565

Query   998    GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   1057
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   26566  GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   26625

Query   1058   ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   1117
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   26626  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   26685

Query   1118   CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   1177
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   26686  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   26745

Query   1178   GACGAGTTCTTCTGAG   1193
               ||||||||||||||||
Sbjct   26746  GACGAGTTCTTCTGAG   26761


>gb|DQ823232.1|      Expression vector mce3, complete sequence
Length=38473

 Score = 1471 bits (796),  Expect = 0.0
 Identities = 796/796 (100%), Gaps = 0/796 (0%)
 Strand=Plus/Plus

Query   398    ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   457
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   35391  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   35450

Query   458    GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   517
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   35451  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   35510

Query   518    GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   577
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   35511  GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   35570

Query   578    CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   637
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   35571  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   35630

Query   638    CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   697
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   35631  CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   35690

Query   698    GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   757
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   35691  GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   35750

Query   758    CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   817
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   35751  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   35810

Query   818    ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   877
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   35811  ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   35870

Query   878    GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   937
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   35871  GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   35930

Query   938    GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   997
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   35931  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   35990

Query   998    GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   1057
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   35991  GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   36050

Query   1058   ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   1117
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Sbjct  36051  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC  36110

Query  1118  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT  1177
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  36111  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT  36170

Query  1178  GACGAGTTCTTCTGAG  1193
             ||||||||||||||||
Sbjct  36171  GACGAGTTCTTCTGAG  36186
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>gb|DQ823231.1| ▨ Expression vector mce2, complete sequence
Length=24799

 Score = 1471 bits (796), Expect = 0.0
 Identities = 796/796 (100%), Gaps = 0/796 (0%)
 Strand=Plus/Plus

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Query  398   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC  457
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  21717  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC  21776

Query  458   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA  517
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  21777  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA  21836

Query  518   GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG  577
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  21837  GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG  21896

Query  578   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG  637
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  21897  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG  21956

Query  638   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG  697
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  21957  CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG  22016

Query  698   GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG  757
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  22017  GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG  22076

Query  758   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC  817
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  22077  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC  22136

Query  818   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA  877
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  22137  ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA  22196

Query  878   GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC  937
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  22197  GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC  22256

Query  938   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT  997
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  22257  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT  22316

Query  998   GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC  1057
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  22317  GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC  22376

Query  1058  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC  1117
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  22377  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC  22436

Query  1118  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT  1177
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  22437  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT  22496

Query  1178  GACGAGTTCTTCTGAG  1193
             ||||||||||||||||
Sbjct  22497  GACGAGTTCTTCTGAG  22512
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>gb|DQ487156.1| Flexi vector pF5K CMV-neo, complete sequence
Length=4594

 Score = 1471 bits (796), Expect = 0.0

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     Identities = 796/796 (100%), Gaps = 0/796 (0%)
     Strand=Plus/Plus

Query   398   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   457
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2409  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   2468

Query   458   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   517
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2469  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   2528

Query   518   GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   577
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2529  GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   2588

Query   578   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   637
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2589  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   2648

Query   638   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   697
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2649  CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   2708

Query   698   GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   757
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2709  GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   2768

Query   758   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   817
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2769  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   2828

Query   818   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   877
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2829  ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   2888

Query   878   GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   937
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2889  GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   2948

Query   938   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   997
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2949  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   3008

Query   998   GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   1057
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3009  GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   3068

Query   1058  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   1117
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3069  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   3128

Query   1118  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   1177
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3129  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   3188

Query   1178  GACGAGTTCTTCTGAG    1193
              ||||||||||||||||
Sbjct   3189  GACGAGTTCTTCTGAG    3204


>gb|DQ487155.1|  Flexi vector pF5A CMV-neo, complete sequence
Length=5591

 Score = 1471 bits (796),  Expect = 0.0
 Identities = 796/796 (100%), Gaps = 0/796 (0%)
 Strand=Plus/Plus

Query   398   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   457
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2366  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   2425

Query   458   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   517
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2426  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   2485

Query   518   GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   577
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2486  GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   2545

Query   578   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   637
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                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2546   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   2605

Query    638   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   697
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2606   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   2665

Query    698   GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   757
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2666   GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   2725

Query    758   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   817
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2726   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   2785

Query    818   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   877
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2786   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   2845

Query    878   GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   937
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2846   GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   2905

Query    938   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   997
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2906   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   2965

Query    998   GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   1057
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2966   GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   3025

Query   1058   ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   1117
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3026   ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   3085

Query   1118   CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   1177
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3086   CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   3145

Query   1178   GACGAGTTCTTCTGAG      1193
                    ||||||||||||||||
Sbjct   3146   GACGAGTTCTTCTGAG      3161
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>gb|DQ487211.1| Flexi Vector pFN10A (ACT), complete sequence
Length=5867

 Score = 1471 bits (796),   Expect = 0.0
 Identities = 796/796 (100%), Gaps = 0/796 (0%)
 Strand=Plus/Plus

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Query    398   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   457
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2642   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   2701

Query    458   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   517
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2702   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   2761

Query    518   GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   577
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2762   GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   2821

Query    578   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   637
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2822   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   2881

Query    638   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   697
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2882   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   2941

Query    698   GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   757
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2942   GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   3001

Query    758   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   817
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3002   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   3061

Query    818   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   877
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                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3062  ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA  3121

Query   878  GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   937
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3122  GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC  3181

Query   938  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   997
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3182  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT  3241

Query   998  GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC  1057
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3242  GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC  3301

Query  1058  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC  1117
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3302  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC  3361

Query  1118  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT  1177
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3362  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT  3421

Query  1178  GACGAGTTCTTCTGAG    1193
                    ||||||||||||||||
Sbjct  3422  GACGAGTTCTTCTGAG    3437


>gb|DQ515893.1|  HIS3/URA3 reporter vector pH3U3, complete sequence
Length=5834

 Score = 1471 bits (796),  Expect = 0.0
 Identities = 796/796 (100%), Gaps = 0/796 (0%)
 Strand=Plus/Minus

Query   398  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   457
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3264  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC  3205

Query   458  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   517
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3204  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA  3145

Query   518  GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   577
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3144  GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG  3085

Query   578  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   637
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3084  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG  3025

Query   638  CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   697
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3024  CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG  2965

Query   698  GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   757
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2964  GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG  2905

Query   758  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   817
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2904  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC  2845

Query   818  ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   877
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2844  ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA  2785

Query   878  GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   937
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2784  GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC  2725

Query   938  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   997
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2724  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT  2665

Query   998  GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC  1057
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2664  GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC  2605

Query  1058  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC  1117
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              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2604   ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC  2545

Query  1118   CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT  1177
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2544   CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT  2485

Query  1178   GACGAGTTCTTCTGAG   1193
              ||||||||||||||||
Sbjct  2484   GACGAGTTCTTCTGAG   2469
```

>gb|DQ408591.1| Transposon mutagenesis vector pG18-STM, complete sequence
Length=7657

 Score = 1471 bits (796),   Expect = 0.0
 Identities = 796/796 (100%), Gaps = 0/796 (0%)
 Strand=Plus/Plus

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Query   398   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   457
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4863   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   4922

Query   458   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   517
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4923   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   4982

Query   518   GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   577
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4983   GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   5042

Query   578   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   637
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  5043   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   5102

Query   638   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   697
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  5103   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   5162

Query   698   GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   757
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  5163   GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   5222

Query   758   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   817
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  5223   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   5282

Query   818   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   877
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  5283   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   5342

Query   878   GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   937
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  5343   GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   5402

Query   938   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   997
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  5403   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   5462

Query   998   GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   1057
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  5463   GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   5522

Query  1058   ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   1117
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  5523   ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   5582

Query  1118   CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   1177
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  5583   CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   5642

Query  1178   GACGAGTTCTTCTGAG   1193
              ||||||||||||||||
Sbjct  5643   GACGAGTTCTTCTGAG   5658
```

>gb|AY817672.1| SIV vector pCLN8, complete sequence
Length=19831

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     Score = 1471 bits (796),  Expect = 0.0
     Identities = 796/796 (100%), Gaps = 0/796 (0%)
     Strand=Plus/Minus

Query   398   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   457
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  14079  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC  14020

Query   458   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   517
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  14019  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA  13960

Query   518   GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   577
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  13959  GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG  13900

Query   578   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   637
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  13899  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG  13840

Query   638   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   697
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  13839  CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG  13780

Query   698   GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   757
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  13779  GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG  13720

Query   758   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   817
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  13719  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC  13660

Query   818   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   877
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  13659  ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA  13600

Query   878   GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   937
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  13599  GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC  13540

Query   938   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   997
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  13539  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT  13480

Query   998   GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC  1057
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  13479  GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC  13420

Query  1058   ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC  1117
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  13419  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC  13360

Query  1118   CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT  1177
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  13359  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT  13300

Query  1178   GACGAGTTCTTCTGAG  1193
              ||||||||||||||||
Sbjct  13299  GACGAGTTCTTCTGAG  13284


>gb|AY266291.1|  Escherichia coli/Mycobacteria shuttle vector pGB9.2, complete
sequence
Length=11441

     Score = 1471 bits (796),  Expect = 0.0
     Identities = 796/796 (100%), Gaps = 0/796 (0%)
     Strand=Plus/Plus

Query   398   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   457
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   334   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   393

Query   458   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   517
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   394   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   453

Query   518   GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   577
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Sbjct   454   GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   513

Query   578   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   637
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   514   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   573

Query   638   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   697
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   574   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   633

Query   698   GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   757
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   634   GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   693

Query   758   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   817
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   694   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   753

Query   818   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   877
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   754   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   813

Query   878   GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   937
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   814   GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   873

Query   938   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   997
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   874   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   933

Query   998   GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   1057
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   934   GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   993

Query   1058  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   1117
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   994   ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   1053

Query   1118  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   1177
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1054  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   1113

Query   1178  GACGAGTTCTTCTGAG   1193
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Sbjct   1114  GACGAGTTCTTCTGAG   1129
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>gb|AY613997.1| Cloning vector pSRalphaneoR, complete sequence
Length=6423

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 Score = 1471 bits (796),  Expect = 0.0
 Identities = 796/796 (100%), Gaps = 0/796 (0%)
 Strand=Plus/Minus

Query   398   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   457
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3088  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   3029

Query   458   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   517
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3028  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   2969

Query   518   GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   577
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2968  GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   2909

Query   578   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   637
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2908  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   2849

Query   638   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   697
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2848  CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   2789

Query   698   GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   757
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Sbjct  2788   GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   2729

Query   758   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC    817
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2728   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   2669

Query   818   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA    877
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2668   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   2609

Query   878   GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC    937
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2608   GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   2549

Query   938   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT    997
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2548   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   2489

Query   998   GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   1057
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2488   GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   2429

Query  1058   ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   1117
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2428   ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   2369

Query  1118   CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   1177
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2368   CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   2309

Query  1178   GACGAGTTCTTCTGAG   1193
              ||||||||||||||||
Sbjct  2308   GACGAGTTCTTCTGAG   2293


 Score = 1057 bits (572),  Expect = 0.0
 Identities = 572/572 (100%), Gaps = 0/572 (0%)
 Strand=Plus/Plus

Query  1200   CCCTCTCCCTccccccccccTAACGTTACTGGCCGAAGCCGCTTGGAATAAGGCCGGTGT   1259
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   101   CCCTCTCCCTCCCCCCCCCCTAACGTTACTGGCCGAAGCCGCTTGGAATAAGGCCGGTGT    160

Query  1260   GCGTTTGTCTATATGTTATTTTCCACCATATTGCCGTCTTTTGGCAATGTGAGGGCCCGG   1319
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   161   GCGTTTGTCTATATGTTATTTTCCACCATATTGCCGTCTTTTGGCAATGTGAGGGCCCGG    220

Query  1320   AAACCTGGCCCTGTCTTCTTGACGAGCATTCCTAGGGGTCTTTCCCCTCTCGCCAAAGGA   1379
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   221   AAACCTGGCCCTGTCTTCTTGACGAGCATTCCTAGGGGTCTTTCCCCTCTCGCCAAAGGA    280

Query  1380   ATGCAAGGTCTGTTGAATGTCGTGAAGGAAGCAGTTCCTCTGGAAGCTTCTTGAAGACAA   1439
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   281   ATGCAAGGTCTGTTGAATGTCGTGAAGGAAGCAGTTCCTCTGGAAGCTTCTTGAAGACAA    340

Query  1440   ACAACGTCTGTAGCGACCCTTTGCAGGCAGCGGAACCCCCCACCTGGCGACAGGTGCCTC   1499
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   341   ACAACGTCTGTAGCGACCCTTTGCAGGCAGCGGAACCCCCCACCTGGCGACAGGTGCCTC    400

Query  1500   TGCGGCCAAAAGCCACGTGTATAAGATACACCTGCAAAGGCGGCACAACCCCAGTGCCAC   1559
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   401   TGCGGCCAAAAGCCACGTGTATAAGATACACCTGCAAAGGCGGCACAACCCCAGTGCCAC    460

Query  1560   GTTGTGAGTTGGATAGTTGTGGAAAGAGTCAAATGGCTCTCCTCAAGCGTATTCAACAAG   1619
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   461   GTTGTGAGTTGGATAGTTGTGGAAAGAGTCAAATGGCTCTCCTCAAGCGTATTCAACAAG    520

Query  1620   GGGCTGAAGGATGCCCAGAAGGTACCCCATTGTATGGGATCTGATCTGGGGCCTCGGTGC   1679
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   521   GGGCTGAAGGATGCCCAGAAGGTACCCCATTGTATGGGATCTGATCTGGGGCCTCGGTGC    580

Query  1680   ACATGCTTTACATGTGTTTAGTCGAGGTTaaaaaaaCGTCTAGGCCCCCCGAACCACGGG   1739
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   581   ACATGCTTTACATGTGTTTAGTCGAGGTTAAAAAAACGTCTAGGCCCCCCGAACCACGGG    640

Query  1740   GACGTGGTTTTCCTTTGAAAAACACGATGATA   1771
              ||||||||||||||||||||||||||||||||
Sbjct   641   GACGTGGTTTTCCTTTGAAAAACACGATGATA    672
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 Score = 1057 bits (572),  Expect = 0.0
 Identities = 572/572 (100%), Gaps = 0/572 (0%)
 Strand=Plus/Plus

Query  1200  CCCTCTCCCTccccccccccTAACGTTACTGGCCGAAGCCGCTTGGAATAAGGCCGGTGT  1259
             |||||||||||          |||||||||||||||||||||||||||||||||||||||
Sbjct  787   CCCTCTCCCTCCCCCCCCCCCTAACGTTACTGGCCGAAGCCGCTTGGAATAAGGCCGGTGT  846

Query  1260  GCGTTTGTCTATATGTTATTTTCCACCATATTGCCGTCTTTTGGCAATGTGAGGGCCCGG  1319
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  847   GCGTTTGTCTATATGTTATTTTCCACCATATTGCCGTCTTTTGGCAATGTGAGGGCCCGG  906

Query  1320  AAACCTGGCCCTGTCTTCTTGACGAGCATTCCTAGGGGTCTTTCCCCTCTCGCCAAAGGA  1379
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  907   AAACCTGGCCCTGTCTTCTTGACGAGCATTCCTAGGGGTCTTTCCCCTCTCGCCAAAGGA  966

Query  1380  ATGCAAGGTCTGTTGAATGTCGTGAAGGAAGCAGTTCCTCTGGAAGCTTCTTGAAGACAA  1439
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  967   ATGCAAGGTCTGTTGAATGTCGTGAAGGAAGCAGTTCCTCTGGAAGCTTCTTGAAGACAA  1026

Query  1440  ACAACGTCTGTAGCGACCCTTTGCAGGCAGCGGAACCCCCCACCTGGCGACAGGTGCCTC  1499
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1027  ACAACGTCTGTAGCGACCCTTTGCAGGCAGCGGAACCCCCCACCTGGCGACAGGTGCCTC  1086

Query  1500  TGCGGCCAAAAGCCACGTGTATAAGATACACCTGCAAAGGCGGCACAACCCCAGTGCCAC  1559
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1087  TGCGGCCAAAAGCCACGTGTATAAGATACACCTGCAAAGGCGGCACAACCCCAGTGCCAC  1146

Query  1560  GTTGTGAGTTGGATAGTTGTGGAAAGAGTCAAATGGCTCTCCTCAAGCGTATTCAACAAG  1619
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1147  GTTGTGAGTTGGATAGTTGTGGAAAGAGTCAAATGGCTCTCCTCAAGCGTATTCAACAAG  1206

Query  1620  GGGCTGAAGGATGCCCAGAAGGTACCCCATTGTATGGGATCTGATCTGGGGCCTCGGTGC  1679
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1207  GGGCTGAAGGATGCCCAGAAGGTACCCCATTGTATGGGATCTGATCTGGGGCCTCGGTGC  1266

Query  1680  ACATGCTTTACATGTGTTTAGTCGAGGTTaaaaaaaCGTCTAGGCCCCCCGAACCACGGG  1739
             |||||||||||||||||||||||||||||       ||||||||||||||||||||||||
Sbjct  1267  ACATGCTTTACATGTGTTTAGTCGAGGTTAAAAAAACGTCTAGGCCCCCCGAACCACGGG  1326

Query  1740  GACGTGGTTTTCCTTTGAAAAACACGATGATA     1771
             ||||||||||||||||||||||||||||||||
Sbjct  1327  GACGTGGTTTTCCTTTGAAAAACACGATGATA     1358


>gb|AY613992.1|  Cloning vector pSRalphaneo, complete sequence
Length=4542

 Score = 1471 bits (796),  Expect = 0.0
 Identities = 796/796 (100%), Gaps = 0/796 (0%)
 Strand=Plus/Minus

Query  398   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC  457
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1207  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC  1148

Query  458   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA  517
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1147  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA  1088

Query  518   GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG  577
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1087  GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG  1028

Query  578   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG  637
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1027  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG  968

Query  638   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG  697
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  967   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG  908

Query  698   GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG  757
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  907   GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG  848

Query  758   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC  817
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  847   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC  788
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Query    818   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   877
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct    787   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   728

Query    878   GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   937
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct    727   GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   668

Query    938   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   997
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct    667   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   608

Query    998   GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   1057
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct    607   GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   548

Query    1058  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   1117
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct    547   ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   488

Query    1118  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   1177
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct    487   CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   428

Query    1178  GACGAGTTCTTCTGAG    1193
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Sbjct    427   GACGAGTTCTTCTGAG    412


>gb|AY286001.1|  Cloning vector pHRE1-km, complete sequence
Length=9037

 Score = 1471 bits (796),  Expect = 0.0
 Identities = 796/796 (100%), Gaps = 0/796 (0%)
 Strand=Plus/Minus

Query    398   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   457
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct    3776  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   3717

Query    458   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   517
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct    3716  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   3657

Query    518   GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   577
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct    3656  GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   3597

Query    578   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   637
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct    3596  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   3537

Query    638   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   697
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct    3536  CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   3477

Query    698   GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   757
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct    3476  GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   3417

Query    758   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   817
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct    3416  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   3357

Query    818   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   877
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct    3356  ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   3297

Query    878   GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   937
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct    3296  GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   3237

Query    938   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   997
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct    3236  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   3177

Query    998   GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   1057
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct    3176  GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   3117
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Query  1058  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC  1117
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3116  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC  3057

Query  1118  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT  1177
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3056  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT  2997

Query  1178  GACGAGTTCTTCTGAG     1193
             ||||||||||||||||
Sbjct  2996  GACGAGTTCTTCTGAG     2981
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>gb|DQ059989.1| ▨ Cloning vector pSCR001, complete sequence
Length=10571

 Score = 1471 bits (796), Expect = 0.0
 Identities = 796/796 (100%), Gaps = 0/796 (0%)
 Strand=Plus/Plus

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Query  398   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC  457
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Sbjct  7019  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC  7078

Query  458   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA  517
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  7079  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA  7138

Query  518   GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG  577
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  7139  GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG  7198

Query  578   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG  637
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  7199  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG  7258

Query  638   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG  697
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  7259  CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG  7318

Query  698   GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG  757
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  7319  GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG  7378

Query  758   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC  817
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  7379  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC  7438

Query  818   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA  877
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  7439  ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA  7498

Query  878   GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC  937
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  7499  GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC  7558

Query  938   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT  997
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  7559  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT  7618

Query  998   GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC  1057
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  7619  GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC  7678

Query  1058  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC  1117
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  7679  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC  7738

Query  1118  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT  1177
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  7739  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT  7798

Query  1178  GACGAGTTCTTCTGAG     1193
             ||||||||||||||||
Sbjct  7799  GACGAGTTCTTCTGAG     7814
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>gb|AY260554.1| Retrotransposon vector MEL/ELM, complete sequence
Length=9945

Sort alignments for this
E value Score Percen
Query start position

Score = 1471 bits (796),   Expect = 0.0
Identities = 796/796 (100%), Gaps = 0/796 (0%)
Strand=Plus/Plus

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Query   398   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   457
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   5600  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   5659

Query   458   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   517
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   5660  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   5719

Query   518   GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   577
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   5720  GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   5779

Query   578   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   637
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   5780  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   5839

Query   638   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   697
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   5840  CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   5899

Query   698   GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   757
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   5900  GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   5959

Query   758   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   817
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   5960  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   6019

Query   818   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   877
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   6020  ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   6079

Query   878   GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   937
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   6080  GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   6139

Query   938   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   997
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   6140  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   6199

Query   998   GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   1057
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   6200  GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   6259

Query   1058  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   1117
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   6260  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   6319

Query   1118  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   1177
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   6320  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   6379

Query   1178  GACGAGTTCTTCTGAG    1193
              ||||||||||||||||
Sbjct   6380  GACGAGTTCTTCTGAG    6395
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Score = 1024 bits (554),   Expect = 0.0
Identities = 559/561 (99%), Gaps = 1/561 (0%)
Strand=Plus/Plus

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Query   1211  CCCCCCCCCTAACGTTACTGGCCGAAGCCGCTTGGAATAAGGCCGGTGTGCGTTTGTCTA   1270
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1249  CCCCCCCCCCTAACGTTACTGGCCGAAGCCGCTTGGAATAAGGCCGGTGTGCGTTTGTCTA   1308

Query   1271  TATGTTATTTTCCACCATATTGCCGTCTTTTGGCAATGTGAGGGCCCGGAAACCTGGCCC   1330
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1309  TATGTTATTTTCCACCATATTGCCGTCTTTTGGCAATGTGAGGGCCCGGAAACCTGGCCC   1368

Query   1331  TGTCTTCTTGACGAGCATTCCTAGGGGTCTTTCCCCTCTCGCCAAAGGAATGCAAGGTCT   1390
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Sbjct   1369   TGTCTTCTTGACGAGCATTCCTAGGGGTCTTTCCCCTCTCGCCAAAGGAATGCAAGGTCT   1428

Query   1391   GTTGAATGTCGTGAAGGAAGCAGTTCCTCTGGAAGCTTCTTGAAGACAAACAACGTCTGT   1450
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1429   GTTGAATGTCGTGAAGGAAGCAGTTCCTCTGGAAGCTTCTTGAAGACAAACAACGTCTGT   1488

Query   1451   AGCGACCCTTTGCAGGCAGCGGAACCCCCCACCTGGCGACAGGTGCCTCTGCGGCCAAAA   1510
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1489   AGCGACCCTTTGCAGGCAGCGGAACCCCCCACCTGGCGACAGGTGCCTCTGCGGCCAAAA   1548

Query   1511   GCCACGTGTATAAGATACACCTGCAAAGGCGGCACAACCCCAGTGCCACGTTGTGAGTTG   1570
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1549   GCCACGTGTATAAGATACACCTGCAAAGGCGGCACAACCCCAGTGCCACGTTGTGAGTTG   1608

Query   1571   GATAGTTGTGGAAAGAGTCAAATGGCTCTCCTCAAGCGTATTCAACAAGGGGCTGAAGGA   1630
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1609   GATAGTTGTGGAAAGAGTCAAATGGCTCTCCTCAAGCGTATTCAACAAGGGGCTGAAGGA   1668

Query   1631   TGCCCAGAAGGTACCCCATTGTATGGGATCTGATCTGGGGCCTCGGTGCACATGCTTTAC   1690
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1669   TGCCCAGAAGGTACCCCATTGTATGGGATCTGATCTGGGGCCTCGGTGCACATGCTTTAC   1728

Query   1691   ATGTGTTTAGTCGAGGTTaaaaaaaCGTCTAGGCCCCCCGAACCACGGGGACGTGGTTTT   1750
               |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Sbjct   1729   ATGTGTTTAGTCGAGGTTAAAAAA-CGTCTAGGCCCCCCGAACCACGGGGACGTGGTTTT   1787

Query   1751   CCTTTGAAAAACACGATGATA     1771
               |||||||||||||||||| |||
Sbjct   1788   CCTTTGAAAAACACGATAATA     1808
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>gb|AY260553.1| ▨ Retrotransposon vector ELM 5, complete sequence
Length=10047

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                                              Sort alignments for this
                                               E value  Score  Percen
                                               Query start position
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 Score = 1471 bits (796),  Expect = 0.0
 Identities = 796/796 (100%), Gaps = 0/796 (0%)
 Strand=Plus/Plus
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Query   398    ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   457
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   5651   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   5710

Query   458    GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   517
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   5711   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   5770

Query   518    GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   577
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   5771   GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   5830

Query   578    CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   637
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   5831   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   5890

Query   638    CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   697
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   5891   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   5950

Query   698    GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   757
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   5951   GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   6010

Query   758    CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   817
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   6011   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   6070

Query   818    ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   877
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   6071   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   6130

Query   878    GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   937
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Sbjct   6131   GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   6190

Query   938    GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   997
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              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  6191   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT  6250

Query   998   GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC  1057
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  6251   GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC  6310

Query  1058   ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC  1117
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  6311   ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC  6370

Query  1118   CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT  1177
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  6371   CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT  6430

Query  1178   GACGAGTTCTTCTGAG    1193
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Sbjct  6431   GACGAGTTCTTCTGAG    6446
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 Score = 1024 bits (554),  Expect = 0.0
 Identities = 559/561 (99%),  Gaps = 1/561 (0%)
 Strand=Plus/Plus
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Query  1211   ccccccccccTAACGTTACTGGCCGAAGCCGCTTGGAATAAGGCCGGTGTGCGTTTGTCTA  1270
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Sbjct  1300   CCCCCCCCCCTAACGTTACTGGCCGAAGCCGCTTGGAATAAGGCCGGTGTGCGTTTGTCTA  1359

Query  1271   TATGTTATTTTCCACCATATTGCCGTCTTTTGGCAATGTGAGGGCCCGGAAACCTGGCCC  1330
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1360   TATGTTATTTTCCACCATATTGCCGTCTTTTGGCAATGTGAGGGCCCGGAAACCTGGCCC  1419

Query  1331   TGTCTTCTTGACGAGCATTCCTAGGGGTCTTTCCCCTCTCGCCAAAGGAATGCAAGGTCT  1390
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1420   TGTCTTCTTGACGAGCATTCCTAGGGGTCTTTCCCCTCTCGCCAAAGGAATGCAAGGTCT  1479

Query  1391   GTTGAATGTCGTGAAGGAAGCAGTTCCTCTGGAAGCTTCTTGAAGACAAACAACGTCTGT  1450
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1480   GTTGAATGTCGTGAAGGAAGCAGTTCCTCTGGAAGCTTCTTGAAGACAAACAACGTCTGT  1539

Query  1451   AGCGACCCTTTGCAGGCAGCGGAACCCCCCACCTGGCGACAGGTGCCTCTGCGGCCAAAA  1510
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1540   AGCGACCCTTTGCAGGCAGCGGAACCCCCCACCTGGCGACAGGTGCCTCTGCGGCCAAAA  1599

Query  1511   GCCACGTGTATAAGATACACCTGCAAAGGCGGCACAACCCCAGTGCCACGTTGTGAGTTG  1570
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1600   GCCACGTGTATAAGATACACCTGCAAAGGCGGCACAACCCCAGTGCCACGTTGTGAGTTG  1659

Query  1571   GATAGTTGTGGAAAGAGTCAAATGGCTCTCCTCAAGCGTATTCAACAAGGGGCTGAAGGA  1630
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1660   GATAGTTGTGGAAAGAGTCAAATGGCTCTCCTCAAGCGTATTCAACAAGGGGCTGAAGGA  1719

Query  1631   TGCCCAGAAGGTACCCCATTGTATGGGATCTGATCTGGGGCCTCGGTGCACATGCTTTAC  1690
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1720   TGCCCAGAAGGTACCCCATTGTATGGGATCTGATCTGGGGCCTCGGTGCACATGCTTTAC  1779

Query  1691   ATGTGTTTAGTCGAGGTTaaaaaaaCGTCTAGGCCCCCCGAACCACGGGGACGTGGTTTT  1750
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Sbjct  1780   ATGTGTTTAGTCGAGGTTAAAAAA-CGTCTAGGCCCCCCGAACCACGGGGACGTGGTTTT  1838

Query  1751   CCTTTGAAAAACACGATGATA    1771
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Sbjct  1839   CCTTTGAAAAACACGATAATA    1859
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>gb|AY037297.1| Synthetic construct erythromycin resistance protein (erm) gene,
partial cds; and streptomycin 3'-phosphotransferase (sph),
bleomycin phosphotransferase (ble), neomycin phosphotransferase
(nptII), and gentamycin resistance protein (aac) genes,
complete cds
Length=7080

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 Score = 1471 bits (796),  Expect = 0.0
 Identities = 796/796 (100%),  Gaps = 0/796 (0%)
 Strand=Plus/Minus
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Query   398   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC  457
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4740   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC  4681
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Query   458   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   517
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   4680  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   4621

Query   518   GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   577
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   4620  GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   4561

Query   578   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   637
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   4560  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   4501

Query   638   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   697
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   4500  CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   4441

Query   698   GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   757
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   4440  GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   4381

Query   758   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   817
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   4380  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   4321

Query   818   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   877
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   4320  ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   4261

Query   878   GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   937
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   4260  GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   4201

Query   938   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   997
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   4200  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   4141

Query   998   GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   1057
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   4140  GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   4081

Query   1058  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   1117
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   4080  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   4021

Query   1118  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   1177
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   4020  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   3961

Query   1178  GACGAGTTCTTCTGAG      1193
              ||||||||||||||||
Sbjct   3960  GACGAGTTCTTCTGAG      3945
```

>gb|AF264696.2| Cloning vector pFB-ERV, complete sequence
Length=11065

Sort alignments for this
E value Score Percen
Query start position

Score = 1471 bits (796), Expect = 0.0
Identities = 796/796 (100%), Gaps = 0/796 (0%)
Strand=Plus/Plus

```
Query   398   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   457
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   7575  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   7634

Query   458   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   517
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   7635  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   7694

Query   518   GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   577
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   7695  GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   7754

Query   578   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   637
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   7755  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   7814
```

```
Query    638   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   697
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   7815   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   7874

Query    698   GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   757
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   7875   GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   7934

Query    758   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   817
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   7935   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   7994

Query    818   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   877
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   7995   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   8054

Query    878   GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   937
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   8055   GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   8114

Query    938   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   997
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   8115   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   8174

Query    998   GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   1057
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   8175   GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   8234

Query   1058   ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   1117
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   8235   ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   8294

Query   1118   CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   1177
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   8295   CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   8354

Query   1178   GACGAGTTCTTCTGAG      1193
               ||||||||||||||||
Sbjct   8355   GACGAGTTCTTCTGAG      8370
```

```
 Score = 1046 bits (566),  Expect = 0.0
 Identities = 571/573 (99%), Gaps = 2/573 (0%)
 Strand=Plus/Plus
```

```
Query   1200   CCCTCTCCCTccccccccccTAACGTTACTGGCCGAAGCCGCTTGGAATAAGGCCGGTGT   1259
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   4968   CCCTCTCCCTCCCCCCCCCCTAACGTTACTGGCCGAAGCCGCTTGGAATAAGGCCGGTGT   5027

Query   1260   GCGTTTGTCTATATGTTATTTTCCACCATATTGCCGTCTTTTGGCAATGTGAGGGCCCGG   1319
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   5028   GCGTTTGTCTATATGTTATTTTCCACCATATTGCCGTCTTTTGGCAATGTGAGGGCCCGG   5087

Query   1320   AAACCTGGCCCTGTCTTCTTGACGAGCATTCCTAGGGGTCTTTCCCCTCTCGCCAAAGGA   1379
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   5088   AAACCTGGCCCTGTCTTCTTGACGAGCATTCCTAGGGGTCTTTCCCCTCTCGCCAAAGGA   5147

Query   1380   ATGCAAGGTCTGTTGAATGTCGTGAAGGAAGCAGTTCCTCTGGAAGCTTCTTGAAGACAA   1439
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   5148   ATGCAAGGTCTGTTGAATGTCGTGAAGGAAGCAGTTCCTCTGGAAGCTTCTTGAAGACAA   5207

Query   1440   ACAACGTCTGTAGCGACCCTTTGCAGGCAGCGGAACCCCCCACCTGGCGACAGGTGCCTC   1499
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   5208   ACAACGTCTGTAGCGACCCTTTGCAGGCAGCGGAACCCCCCACCTGGCGACAGGTGCCTC   5267

Query   1500   TGCGGCCAAAAGCCACGTGTATAAGATACACCTGCAAAGGCGGCACAACCCCAGTGCCAC   1559
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   5268   TGCGGCCAAAAGCCACGTGTATAAGATACACCTGCAAAGGCGGCACAACCCCAGTGCCAC   5327

Query   1560   GTTGTGAGTTGGATAGTTGTGGAAAGAGTCAAATGGCTCTCCTCAAGCGTATTCAACAAG   1619
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   5328   GTTGTGAGTTGGATAGTTGTGGAAAGAGTCAAATGGCTCTCCTCAAGCGTATTCAACAAG   5387

Query   1620   GGGCTGAAGGATGCCCAGAAGGTACCCCATTGTATGGGATCTGATCTGGGGCCTCGGTGC   1679
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   5388   GGGCTGAAGGATGCCCAGAAGGTACCCCATTGTATGGGATCTGATCTGGGGCCTCGGTGC   5447

Query   1680   ACATGCTTTACATGTGTTTAGTCGAGGTTaaaaaaaCGTCTAGGCCCCCCGAACCACGGG   1739
               ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
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Sbjct   5448   ACATGCTTTACATGTGTTTAGTCGAGGTTAAAAAA-CGTCTAGGCCCCCCGAACCACGGG   5506

Query   1740   GACGTGGTTTTCCTTTGAAAAACACGAT-GATA    1771
               |||||||||||||||||||||||||||| ||||
Sbjct   5507   GACGTGGTTTTCCTTTGAAAAACACGATCGATA    5539
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 Score = 913 bits (494), Expect = 0.0
 Identities = 497/498 (99%), Gaps = 1/498 (0%)
 Strand=Plus/Plus

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Query   1274   GTTATTTTCCACCATATTGCCGTCTTTTGGCAATGTGAGGGCCCGGAAACCTGGCCCTGT   1333
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   6975   GTTATTTTCCACCATATTGCCGTCTTTTGGCAATGTGAGGGCCCGGAAACCTGGCCCTGT   7034

Query   1334   CTTCTTGACGAGCATTCCTAGGGGTCTTTCCCCTCTCGCCAAAGGAATGCAAGGTCTGTT   1393
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   7035   CTTCTTGACGAGCATTCCTAGGGGTCTTTCCCCTCTCGCCAAAGGAATGCAAGGTCTGTT   7094

Query   1394   GAATGTCGTGAAGGAAGCAGTTCCTCTGGAAGCTTCTTGAAGACAAACAACGTCTGTAGC   1453
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   7095   GAATGTCGTGAAGGAAGCAGTTCCTCTGGAAGCTTCTTGAAGACAAACAACGTCTGTAGC   7154

Query   1454   GACCCTTTGCAGGCAGCGGAACCCCCCACCTGGCGACAGGTGCCTCTGCGGCCAAAAGCC   1513
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   7155   GACCCTTTGCAGGCAGCGGAACCCCCCACCTGGCGACAGGTGCCTCTGCGGCCAAAAGCC   7214

Query   1514   ACGTGTATAAGATACACCTGCAAAGGCGGCACAACCCCAGTGCCACGTTGTGAGTTGGAT   1573
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   7215   ACGTGTATAAGATACACCTGCAAAGGCGGCACAACCCCAGTGCCACGTTGTGAGTTGGAT   7274

Query   1574   AGTTGTGGAAAGAGTCAAATGGCTCTCCTCAAGCGTATTCAACAAGGGGCTGAAGGATGC   1633
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   7275   AGTTGTGGAAAGAGTCAAATGGCTCTCCTCAAGCGTATTCAACAAGGGGCTGAAGGATGC   7334

Query   1634   CCAGAAGGTACCCCATTGTATGGGATCTGATCTGGGGCCTCGGTGCACATGCTTTACATG   1693
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   7335   CCAGAAGGTACCCCATTGTATGGGATCTGATCTGGGGCCTCGGTGCACATGCTTTACATG   7394

Query   1694   TGTTTAGTCGAGGTTaaaaaaaCGTCTAGGCCCCCCGAACCACGGGGACGTGGTTTTCCT   1753
               |||||||||||||||| ||||||| |||||||||||||||||||||||||||||||||||
Sbjct   7395   TGTTTAGTCGAGGTTAAAAAA-CGTCTAGGCCCCCCGAACCACGGGGACGTGGTTTTCCT   7453

Query   1754   TTGAAAAACACGATGATA    1771
               ||||||||||||||||||
Sbjct   7454   TTGAAAAACACGATGATA    7471
```

>gb|DQ092437.1| Insertion vector pWSMK-T, complete sequence
Length=15969

 Score = 1471 bits (796), Expect = 0.0
 Identities = 796/796 (100%), Gaps = 0/796 (0%)
 Strand=Plus/Plus

```
Query   398    ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   457
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   7376   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   7435

Query   458    GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   517
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   7436   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   7495

Query   518    GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   577
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   7496   GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   7555

Query   578    CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   637
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   7556   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   7615

Query   638    CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   697
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   7616   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   7675

Query   698    GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   757
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   7676   GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   7735
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Query    758   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   817
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   7736   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   7795

Query    818   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   877
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   7796   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   7855

Query    878   GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   937
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   7856   GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   7915

Query    938   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   997
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   7916   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   7975

Query    998   GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   1057
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   7976   GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   8035

Query   1058   ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   1117
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   8036   ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   8095

Query   1118   CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   1177
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   8096   CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   8155

Query   1178   GACGAGTTCTTCTGAG     1193
               ||||||||||||||||
Sbjct   8156   GACGAGTTCTTCTGAG     8171


>gb|AF504908.1|  Cloning vector pBBRT, complete sequence
Length=5973

 Score = 1471 bits (796),  Expect = 0.0
 Identities = 796/796 (100%), Gaps = 0/796 (0%)
 Strand=Plus/Minus

Query    398   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   457
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   4687   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   4628

Query    458   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   517
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   4627   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   4568

Query    518   GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   577
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   4567   GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   4508

Query    578   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   637
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   4507   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   4448

Query    638   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   697
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   4447   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   4388

Query    698   GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   757
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   4387   GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   4328

Query    758   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   817
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   4327   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   4268

Query    818   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   877
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   4267   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   4208

Query    878   GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   937
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   4207   GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   4148

Query    938   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   997
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   4147   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   4088
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Query   998   GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   1057
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   4087  GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   4028

Query   1058  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   1117
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   4027  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   3968

Query   1118  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   1177
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3967  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   3908

Query   1178  GACGAGTTCTTCTGAG   1193
              ||||||||||||||||
Sbjct   3907  GACGAGTTCTTCTGAG   3892


>gb|AY062236.1|  Transformation vector pRLE6, complete sequence
Length=5844

 Score = 1471 bits (796),  Expect = 0.0
 Identities = 796/796 (100%), Gaps = 0/796 (0%)
 Strand=Plus/Plus

Query   398   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   457
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   366   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   425

Query   458   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   517
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   426   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   485

Query   518   GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   577
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   486   GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   545

Query   578   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   637
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   546   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   605

Query   638   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   697
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   606   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   665

Query   698   GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   757
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   666   GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   725

Query   758   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   817
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   726   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   785

Query   818   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   877
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   786   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   845

Query   878   GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   937
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   846   GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   905

Query   938   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   997
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   906   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   965

Query   998   GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   1057
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   966   GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   1025

Query   1058  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   1117
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1026  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   1085

Query   1118  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   1177
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1086  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   1145

Query   1178  GACGAGTTCTTCTGAG   1193
              ||||||||||||||||
Sbjct   1146  GACGAGTTCTTCTGAG   1161
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>gb|AF416990.1|  Synthetic construct plasmid pcDNA3-Rluc, complete sequence
Length=6394

 Score = 1471 bits (796),  Expect = 0.0
 Identities = 796/796 (100%), Gaps = 0/796 (0%)
 Strand=Plus/Plus

Query  398   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC  457
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3099  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC  3158

Query  458   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA  517
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3159  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA  3218

Query  518   GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG  577
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3219  GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG  3278

Query  578   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG  637
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3279  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG  3338

Query  638   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG  697
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3339  CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG  3398

Query  698   GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG  757
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3399  GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG  3458

Query  758   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC  817
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3459  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC  3518

Query  818   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA  877
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3519  ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA  3578

Query  878   GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC  937
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3579  GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC  3638

Query  938   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT  997
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3639  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT  3698

Query  998   GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC  1057
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3699  GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC  3758

Query  1058  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC  1117
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3759  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC  3818

Query  1118  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT  1177
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3819  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT  3878

Query  1178  GACGAGTTCTTCTGAG    1193
             ||||||||||||||||
Sbjct  3879  GACGAGTTCTTCTGAG    3894


>gb|AY181092.1|  Synthetic construct S1 promoter-nptII gene-S3 terminator cassett
Length=1688

 Score = 1471 bits (796),  Expect = 0.0
 Identities = 796/796 (100%), Gaps = 0/796 (0%)
 Strand=Plus/Plus

Query  398   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC  457
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  545   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC  604

Query  458   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA  517
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  605   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA  664
```

```
Query  518   GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   577
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  665   GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   724

Query  578   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   637
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  725   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   784

Query  638   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   697
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  785   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   844

Query  698   GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   757
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  845   GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   904

Query  758   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   817
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  905   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   964

Query  818   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   877
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  965   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   1024

Query  878   GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   937
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1025  GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   1084

Query  938   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   997
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1085  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   1144

Query  998   GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   1057
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1145  GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   1204

Query  1058  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   1117
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1205  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   1264

Query  1118  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   1177
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1265  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   1324

Query  1178  GACGAGTTCTTCTGAG     1193
             ||||||||||||||||
Sbjct  1325  GACGAGTTCTTCTGAG     1340
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>gb|AY159034.1| Cloning vector pPLEX-4004, complete sequence
Length=12880

 Score = 1471 bits (796), Expect = 0.0
 Identities = 796/796 (100%), Gaps = 0/796 (0%)
 Strand=Plus/Plus

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Query  398    ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   457
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  11745  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   11804

Query  458    GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   517
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  11805  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   11864

Query  518    GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   577
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  11865  GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   11924

Query  578    CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   637
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  11925  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   11984

Query  638    CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   697
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  11985  CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   12044

Query  698    GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   757
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  12045  GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   12104
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```
Query   758    CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   817
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   12105  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   12164

Query   818    ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   877
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   12165  ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   12224

Query   878    GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   937
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   12225  GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   12284

Query   938    GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   997
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   12285  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   12344

Query   998    GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   1057
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   12345  GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   12404

Query   1058   ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   1117
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   12405  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   12464

Query   1118   CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   1177
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   12465  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   12524

Query   1178   GACGAGTTCTTCTGAG    1193
               ||||||||||||||||
Sbjct   12525  GACGAGTTCTTCTGAG    12540


>gb|AY159033.1|  Cloning vector pPLEX-4003, complete sequence
Length=12388

 Score = 1471 bits (796),  Expect = 0.0
 Identities = 796/796 (100%), Gaps = 0/796 (0%)
 Strand=Plus/Plus

Query   398    ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   457
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   11253  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   11312

Query   458    GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   517
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   11313  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   11372

Query   518    GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   577
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   11373  GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   11432

Query   578    CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   637
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   11433  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   11492

Query   638    CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   697
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   11493  CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   11552

Query   698    GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   757
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   11553  GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   11612

Query   758    CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   817
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   11613  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   11672

Query   818    ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   877
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   11673  ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   11732

Query   878    GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   937
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   11733  GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   11792

Query   938    GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   997
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Sbjct  11793  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT  11852

Query  998    GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC  1057
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  11853  GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC  11912

Query  1058   ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC  1117
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  11913  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC  11972

Query  1118   CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT  1177
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  11973  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT  12032

Query  1178   GACGAGTTCTTCTGAG  1193
              ||||||||||||||||
Sbjct  12033  GACGAGTTCTTCTGAG  12048
```

>gb|AY159032.1| ▨ Cloning vector pPLEX-4002, complete sequence
Length=12825

 Score = 1471 bits (796), Expect = 0.0
 Identities = 796/796 (100%), Gaps = 0/796 (0%)
 Strand=Plus/Plus

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Query  398    ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC  457
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  11690  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC  11749

Query  458    GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA  517
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  11750  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA  11809

Query  518    GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG  577
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  11810  GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG  11869

Query  578    CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG  637
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  11870  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG  11929

Query  638    CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG  697
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  11930  CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG  11989

Query  698    GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG  757
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  11990  GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG  12049

Query  758    CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC  817
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  12050  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC  12109

Query  818    ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA  877
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  12110  ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA  12169

Query  878    GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC  937
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  12170  GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC  12229

Query  938    GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT  997
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  12230  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT  12289

Query  998    GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC  1057
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  12290  GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC  12349

Query  1058   ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC  1117
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  12350  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC  12409

Query  1118   CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT  1177
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  12410  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT  12469

Query  1178   GACGAGTTCTTCTGAG  1193
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                        ||||||||||||||||||
Sbjct   12470   GACGAGTTCTTCTGAG   12485
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>gb|AY159031.1| ▨ Cloning vector pPLEX-4001, complete sequence
Length=12377

 Score = 1471 bits (796), Expect = 0.0
 Identities = 796/796 (100%), Gaps = 0/796 (0%)
 Strand=Plus/Plus

```
Query   398    ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   457
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   11242  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   11301

Query   458    GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   517
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   11302  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   11361

Query   518    GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   577
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   11362  GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   11421

Query   578    CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   637
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   11422  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   11481

Query   638    CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   697
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   11482  CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   11541

Query   698    GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   757
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   11542  GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   11601

Query   758    CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   817
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   11602  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   11661

Query   818    ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   877
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   11662  ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   11721

Query   878    GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   937
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   11722  GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   11781

Query   938    GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   997
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   11782  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   11841

Query   998    GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   1057
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   11842  GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   11901

Query   1058   ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   1117
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   11902  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   11961

Query   1118   CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   1177
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   11962  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   12021

Query   1178   GACGAGTTCTTCTGAG   1193
               ||||||||||||||||
Sbjct   12022  GACGAGTTCTTCTGAG   12037
```

>gb|AY159029.1| ▨ Cloning vector pPLEX-501, complete sequence
Length=10858

 Score = 1471 bits (796), Expect = 0.0
 Identities = 796/796 (100%), Gaps = 0/796 (0%)
 Strand=Plus/Plus

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Query   398    ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   457
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   9723   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   9782
```

```
Query   458    GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA    517
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   9783   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA    9842

Query   518    GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG    577
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   9843   GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG    9902

Query   578    CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG    637
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   9903   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG    9962

Query   638    CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG    697
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   9963   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG    10022

Query   698    GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG    757
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   10023  GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG    10082

Query   758    CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC    817
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   10083  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC    10142

Query   818    ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA    877
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   10143  ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA    10202

Query   878    GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC    937
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   10203  GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC    10262

Query   938    GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT    997
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   10263  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT    10322

Query   998    GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC    1057
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   10323  GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC    10382

Query   1058   ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC    1117
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   10383  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC    10442

Query   1118   CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT    1177
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   10443  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT    10502

Query   1178   GACGAGTTCTTCTGAG    1193
               ||||||||||||||||
Sbjct   10503  GACGAGTTCTTCTGAG    10518
```

>gb|AY159020.1| ▨ Cloning vector pPLEX-505, complete sequence
Length=10862

  Score = 1471 bits (796), Expect = 0.0
  Identities = 796/796 (100%), Gaps = 0/796 (0%)
  Strand=Plus/Plus

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Query   398    ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC    457
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   9727   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC    9786

Query   458    GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA    517
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   9787   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA    9846

Query   518    GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG    577
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   9847   GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG    9906

Query   578    CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG    637
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   9907   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG    9966

Query   638    CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG    697
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Sbjct   9967   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   10026

Query   698    GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   757
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   10027  GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   10086

Query   758    CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   817
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   10087  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   10146

Query   818    ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   877
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   10147  ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   10206

Query   878    GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   937
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   10207  GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   10266

Query   938    GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   997
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   10267  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   10326

Query   998    GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   1057
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   10327  GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   10386

Query   1058   ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   1117
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   10387  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   10446

Query   1118   CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   1177
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   10447  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   10506

Query   1178   GACGAGTTCTTCTGAG   1193
               ||||||||||||||||
Sbjct   10507  GACGAGTTCTTCTGAG   10522
```

>gb|AY048743.1| Template plasmid pKD4, complete sequence
Length=3267

 Score = 1471 bits (796), Expect = 0.0
 Identities = 796/796 (100%), Gaps = 0/796 (0%)
 Strand=Plus/Plus

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Query   398    ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   457
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   459    ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   518

Query   458    GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   517
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   519    GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   578

Query   518    GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   577
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   579    GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   638

Query   578    CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   637
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   639    CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   698

Query   638    CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   697
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   699    CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   758

Query   698    GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   757
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   759    GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   818

Query   758    CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   817
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   819    CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   878

Query   818    ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   877
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   879    ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   938

Query   878    GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   937
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Sbjct   939   GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   998

Query   938   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   997
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   999   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   1058

Query   998   GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   1057
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1059  GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   1118

Query   1058  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   1117
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1119  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   1178

Query   1118  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   1177
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1179  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   1238

Query   1178  GACGAGTTCTTCTGAG   1193
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Sbjct   1239  GACGAGTTCTTCTGAG   1254
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>gb|AY237648.1| ▨ Cloning vector pHR50, complete sequence
Length=11973

 Score = 1471 bits (796), Expect = 0.0
 Identities = 796/796 (100%), Gaps = 0/796 (0%)
 Strand=Plus/Minus

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Query   398   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   457
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3776  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   3717

Query   458   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   517
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3716  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   3657

Query   518   GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   577
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3656  GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   3597

Query   578   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   637
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3596  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   3537

Query   638   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   697
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3536  CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   3477

Query   698   GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   757
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3476  GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   3417

Query   758   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   817
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3416  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   3357

Query   818   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   877
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3356  ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   3297

Query   878   GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   937
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3296  GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   3237

Query   938   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   997
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3236  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   3177

Query   998   GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   1057
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3176  GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   3117

Query   1058  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   1117
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3116  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   3057

Query   1118  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   1177
```

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              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3056   CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   2997

Query  1178   GACGAGTTCTTCTGAG    1193
              ||||||||||||||||
Sbjct  2996   GACGAGTTCTTCTGAG    2981
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>gb|AY237649.1| Cloning vector pHR3-km, complete sequence
Length=6762

  Score = 1471 bits (796), Expect = 0.0
  Identities = 796/796 (100%), Gaps = 0/796 (0%)
  Strand=Plus/Minus

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Query   398   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC    457
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3776   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   3717

Query   458   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA    517
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3716   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   3657

Query   518   GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG    577
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Sbjct  3656   GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   3597

Query   578   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG    637
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3596   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   3537

Query   638   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG    697
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Sbjct  3536   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   3477

Query   698   GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG    757
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Sbjct  3476   GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   3417

Query   758   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC    817
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Sbjct  3416   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   3357

Query   818   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA    877
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Sbjct  3356   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   3297

Query   878   GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC    937
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3296   GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   3237

Query   938   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT    997
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Sbjct  3236   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   3177

Query   998   GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   1057
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Sbjct  3176   GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   3117

Query  1058   ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   1117
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Sbjct  3116   ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   3057

Query  1118   CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   1177
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Sbjct  3056   CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   2997

Query  1178   GACGAGTTCTTCTGAG   1193
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Sbjct  2996   GACGAGTTCTTCTGAG   2981
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>gb|AY265466.1| Shuttle vector pAM2770, complete sequence
Length=8384

  Score = 1471 bits (796), Expect = 0.0
  Identities = 796/796 (100%), Gaps = 0/796 (0%)
  Strand=Plus/Plus

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Query   398   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC    457
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Sbjct   739     ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   798

Query   458     GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   517
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Sbjct   799     GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   858

Query   518     GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   577
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Sbjct   859     GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   918

Query   578     CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   637
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Sbjct   919     CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   978

Query   638     CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   697
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Sbjct   979     CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   1038

Query   698     GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   757
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Sbjct   1039    GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   1098

Query   758     CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   817
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1099    CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   1158

Query   818     ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   877
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Sbjct   1159    ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   1218

Query   878     GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   937
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Sbjct   1219    GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   1278

Query   938     GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   997
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Sbjct   1279    GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   1338

Query   998     GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   1057
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1339    GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   1398

Query   1058    ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   1117
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Sbjct   1399    ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   1458

Query   1118    CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   1177
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Sbjct   1459    CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   1518

Query   1178    GACGAGTTCTTCTGAG    1193
                ||||||||||||||||
Sbjct   1519    GACGAGTTCTTCTGAG    1534


>gb|AF346624.1|AF346624   RAGE vector pRIG1, complete sequence
Length=6836

 Score = 1471 bits (796),   Expect = 0.0
 Identities = 796/796 (100%), Gaps = 0/796 (0%)
 Strand=Plus/Plus

Query   398     ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   457
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Sbjct   3847    ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   3906

Query   458     GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   517
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3907    GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   3966

Query   518     GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   577
                |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Sbjct   3967    GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   4026

Query   578     CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   637
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   4027    CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   4086

Query   638     CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   697
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Sbjct  4087    CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG    4146

Query   698    GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG    757
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4147    GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG    4206

Query   758    CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC    817
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4207    CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC    4266

Query   818    ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA    877
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4267    ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA    4326

Query   878    GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC    937
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4327    GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC    4386

Query   938    GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT    997
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4387    GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT    4446

Query   998    GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC    1057
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Sbjct  4447    GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC    4506

Query  1058    ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC    1117
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Sbjct  4507    ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC    4566

Query  1118    CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT    1177
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Sbjct  4567    CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT    4626

Query  1178    GACGAGTTCTTCTGAG     1193
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Sbjct  4627    GACGAGTTCTTCTGAG     4642
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>emb|AL671256.1|TBN19B2 [image] Trypanosoma brucei VO2 VSG expression site BAC
Length=137759

 Score = 1471 bits (796), Expect = 0.0
 Identities = 796/796 (100%), Gaps = 0/796 (0%)
 Strand=Plus/Plus

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Query   398    ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC    457
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Sbjct 117684   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC    1177

Query   458    GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA    517
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Sbjct 117744   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA    1178

Query   518    GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG    577
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 117804   GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG    1178

Query   578    CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG    637
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Sbjct 117864   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG    1179

Query   638    CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG    697
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 117924   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG    1179

Query   698    GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG    757
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 117984   GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG    1180

Query   758    CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC    817
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 118044   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC    1181

Query   818    ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA    877
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Query   878    GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   937
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Sbjct   118164 GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   1182

Query   938    GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   997
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Sbjct   118224 GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   1182

Query   998    GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   1057
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Sbjct   118284 GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   1183

Query   1058   ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   1117
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Sbjct   118344 ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   1184

Query   1118   CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   1177
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Sbjct   118404 CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   1184

Query   1178   GACGAGTTCTTCTGAG   1193
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>gb|AF286462.1|AF286462  Promoter probe vector pPROBE'-gfp[LVA], complete sequenc
Length=7385

 Score = 1471 bits (796),  Expect = 0.0
 Identities = 796/796 (100%), Gaps = 0/796 (0%)
 Strand=Plus/Minus

Query   398    ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   457
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Sbjct   6928   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   6869

Query   458    GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   517
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Sbjct   6868   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   6809

Query   518    GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   577
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Sbjct   6808   GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   6749

Query   578    CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   637
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Sbjct   6748   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   6689

Query   638    CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   697
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Sbjct   6688   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   6629

Query   698    GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   757
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Sbjct   6628   GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   6569

Query   758    CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   817
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Sbjct   6568   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   6509

Query   818    ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   877
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Sbjct   6508   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   6449

Query   878    GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   937
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Sbjct   6448   GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   6389

Query   938    GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   997
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Sbjct   6388   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   6329

Query   998    GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   1057
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Sbjct   6328   GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   6269

Query   1058   ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   1117
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Query  1118  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT  1177
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Sbjct  6208  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT  6149

Query  1178  GACGAGTTCTTCTGAG  1193
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Sbjct  6148  GACGAGTTCTTCTGAG  6133
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>gb|AF286461.1|AF286461 Promoter probe vector pPROBE-gfp[LVA], complete sequence
Length=7382

 Score = 1471 bits (796), Expect = 0.0
 Identities = 796/796 (100%), Gaps = 0/796 (0%)
 Strand=Plus/Minus

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Query  398   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC  457
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Sbjct  6925  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC  6866

Query  458   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA  517
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Sbjct  6865  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA  6806

Query  518   GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG  577
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Sbjct  6805  GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG  6746

Query  578   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG  637
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  6745  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG  6686

Query  638   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG  697
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Query  698   GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG  757
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Sbjct  6625  GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG  6566

Query  758   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC  817
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Sbjct  6565  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC  6506

Query  818   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA  877
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Sbjct  6505  ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA  6446

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Sbjct  6445  GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC  6386

Query  938   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT  997
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Sbjct  6385  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT  6326

Query  998   GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC  1057
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Sbjct  6325  GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC  6266

Query  1058  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC  1117
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Sbjct  6265  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC  6206

Query  1118  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT  1177
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  6205  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT  6146

Query  1178  GACGAGTTCTTCTGAG  1193
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Sbjct  6145  GACGAGTTCTTCTGAG  6130
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>gb|AF286460.1|AF286460 Promoter probe vector pPROBE'-gfp[ASV], complete sequenc
Length=7385

 Score = 1471 bits (796), Expect = 0.0
 Identities = 796/796 (100%), Gaps = 0/796 (0%)
 Strand=Plus/Minus

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Query   398   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   457
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Sbjct   6928  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   6869

Query   458   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   517
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Sbjct   6868  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   6809

Query   518   GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   577
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Sbjct   6808  GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   6749

Query   578   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   637
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Sbjct   6748  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   6689

Query   638   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   697
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Sbjct   6688  CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   6629

Query   698   GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   757
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Sbjct   6628  GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   6569

Query   758   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   817
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Sbjct   6568  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   6509

Query   818   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   877
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Sbjct   6508  ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   6449

Query   878   GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   937
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Sbjct   6448  GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   6389

Query   938   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   997
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Sbjct   6388  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   6329

Query   998   GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   1057
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   6328  GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   6269

Query   1058  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   1117
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   6268  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   6209

Query   1118  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   1177
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   6208  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   6149

Query   1178  GACGAGTTCTTCTGAG     1193
              ||||||||||||||||
Sbjct   6148  GACGAGTTCTTCTGAG     6133
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>gb|AF286459.1|AF286459 Promoter probe vector pPROBE-gfp[ASV], complete sequence
Length=7382

 Score = 1471 bits (796), Expect = 0.0
 Identities = 796/796 (100%), Gaps = 0/796 (0%)
 Strand=Plus/Minus

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Query   398   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   457
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   6925  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   6866

Query   458   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   517
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Sbjct   6865  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   6806

Query   518   GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   577
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Sbjct   6805  GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   6746

Query   578   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   637
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Query   698   GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   757
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Sbjct   6625  GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   6566

Query   758   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   817
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Sbjct   6445  GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   6386

Query   938   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   997
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Sbjct   6385  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   6326

Query   998   GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   1057
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   6325  GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   6266

Query   1058  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   1117
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Query   1118  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   1177
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Sbjct   6205  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   6146

Query   1178  GACGAGTTCTTCTGAG    1193
              ||||||||||||||||
Sbjct   6145  GACGAGTTCTTCTGAG    6130
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>gb|AF286458.1|AF286458   Promoter probe vector pPROBE'-gfp[AAV], complete sequenc
Length=7385

 Score = 1471 bits (796),   Expect = 0.0
 Identities = 796/796 (100%), Gaps = 0/796 (0%)
 Strand=Plus/Minus

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Query   398   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   457
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Query   458   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   517
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Sbjct   6868  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   6809

Query   518   GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   577
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Query   578   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   637
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Query   638   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   697
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Query   698   GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   757
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Query   758   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   817
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Sbjct   6568  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   6509

Query   818   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   877
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Sbjct   6448   GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   6389

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Sbjct   6388   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   6329

Query   998    GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   1057
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   6328   GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   6269

Query   1058   ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   1117
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Sbjct   6268   ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   6209

Query   1118   CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   1177
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Sbjct   6208   CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   6149

Query   1178   GACGAGTTCTTCTGAG   1193
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Sbjct   6148   GACGAGTTCTTCTGAG   6133


>gb|AF286457.1|AF286457  Promoter probe vector pPROBE-gfp[AAV], complete sequence
Length=7382

 Score = 1471 bits (796),  Expect = 0.0
 Identities = 796/796 (100%), Gaps = 0/796 (0%)
 Strand=Plus/Minus

Query   398    ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   457
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   6925   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   6866

Query   458    GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   517
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Sbjct   6865   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   6806

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Query   578    CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   637
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Query   638    CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   697
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Query   698    GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   757
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Query   758    CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   817
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Sbjct   6565   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   6506

Query   818    ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   877
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Query   878    GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   937
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Query   938    GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   997
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Sbjct   6385   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   6326

Query   998    GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   1057
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Query   1058   ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   1117
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Sbjct  6205  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT  6146

Query  1178  GACGAGTTCTTCTGAG  1193
             ||||||||||||||||
Sbjct  6145  GACGAGTTCTTCTGAG  6130
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>gb|AF286456.1|AF286456 Promoter probe vector pPROBE'-gfp[tagless], complete seq
Length=7343

 Score = 1471 bits (796), Expect = 0.0
 Identities = 796/796 (100%), Gaps = 0/796 (0%)
 Strand=Plus/Minus

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Query   458  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   517
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Sbjct  6826  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA  6767

Query   518  GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   577
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Sbjct  6766  GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG  6707

Query   578  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   637
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Sbjct  6706  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG  6647

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Sbjct  6646  CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG  6587

Query   698  GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   757
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Query   758  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   817
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Sbjct  6466  ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA  6407

Query   878  GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   937
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Sbjct  6406  GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC  6347

Query   938  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   997
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  6346  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT  6287

Query   998  GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC  1057
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  6286  GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC  6227

Query  1058  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC  1117
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  6226  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC  6167

Query  1118  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT  1177
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  6166  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT  6107

Query  1178  GACGAGTTCTTCTGAG  1193
             ||||||||||||||||
Sbjct  6106  GACGAGTTCTTCTGAG  6091
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>gb|AF286455.1|AF286455 Promoter probe vector pPROBE-gfp[tagless], complete sequ
Length=7340

 Score = 1471 bits (796), Expect = 0.0
 Identities = 796/796 (100%), Gaps = 0/796 (0%)
 Strand=Plus/Minus

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Query   398   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   457
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   6883  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   6824

Query   458   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   517
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   6823  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   6764

Query   518   GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   577
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   6763  GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   6704

Query   578   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   637
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   6703  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   6644

Query   638   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   697
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   6643  CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   6584

Query   698   GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   757
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   6583  GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   6524

Query   758   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   817
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   6523  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   6464

Query   818   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   877
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   6463  ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   6404

Query   878   GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   937
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   6403  GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   6344

Query   938   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   997
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   6343  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   6284

Query   998   GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   1057
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   6283  GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   6224

Query   1058  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   1117
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   6223  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   6164

Query   1118  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   1177
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   6163  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   6104

Query   1178  GACGAGTTCTTCTGAG      1193
              ||||||||||||||||
Sbjct   6103  GACGAGTTCTTCTGAG      6088
```

>gb|AF286454.1|AF286454 Promoter probe vector pPROBE-NT', complete sequence
Length=6810

 Score = 1471 bits (796), Expect = 0.0
 Identities = 796/796 (100%), Gaps = 0/796 (0%)
 Strand=Plus/Minus

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Query   398   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   457
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   6353  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   6294

Query   458   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   517
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   6293  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   6234

Query   518   GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   577
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   6233  GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   6174

Query   578   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   637
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   6173  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   6114
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Query   638   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   697
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   6113  CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   6054

Query   698   GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   757
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   6053  GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   5994

Query   758   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   817
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   5993  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   5934

Query   818   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   877
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   5933  ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   5874

Query   878   GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   937
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   5873  GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   5814

Query   938   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   997
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   5813  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   5754

Query   998   GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   1057
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   5753  GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   5694

Query   1058  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   1117
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   5693  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   5634

Query   1118  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   1177
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   5633  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   5574

Query   1178  GACGAGTTCTTCTGAG      1193
              ||||||||||||||||
Sbjct   5573  GACGAGTTCTTCTGAG      5558
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>gb|AF286453.1|AF286453 Promoter probe vector pPROBE-NT, complete sequence
Length=6807

 Score = 1471 bits (796), Expect = 0.0
 Identities = 796/796 (100%), Gaps = 0/796 (0%)
 Strand=Plus/Minus

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Query   398   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   457
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   6350  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   6291

Query   458   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   517
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   6290  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   6231

Query   518   GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   577
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   6230  GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   6171

Query   578   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   637
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   6170  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   6111

Query   638   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   697
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   6110  CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   6051

Query   698   GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   757
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   6050  GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   5991

Query   758   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   817
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   5990  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   5931

Query   818   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   877
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   5930  ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   5871
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Query    878   GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   937
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   5870   GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   5811

Query    938   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   997
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   5810   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   5751

Query    998   GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   1057
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   5750   GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   5691

Query   1058   ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   1117
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   5690   ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   5631

Query   1118   CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   1177
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   5630   CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   5571

Query   1178   GACGAGTTCTTCTGAG      1193
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Sbjct   5570   GACGAGTTCTTCTGAG      5555


>gb|AY962288.1|  Low threshold vector pLTSUB-302, complete sequence
Length=4719

 Score = 1471 bits (796),  Expect = 0.0
 Identities = 796/796 (100%), Gaps = 0/796 (0%)
 Strand=Plus/Plus

Query    398   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   457
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3103   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   3162

Query    458   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   517
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3163   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   3222

Query    518   GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   577
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3223   GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   3282

Query    578   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   637
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3283   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   3342

Query    638   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   697
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3343   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   3402

Query    698   GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   757
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3403   GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   3462

Query    758   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   817
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3463   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   3522

Query    818   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   877
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3523   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   3582

Query    878   GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   937
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3583   GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   3642

Query    938   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   997
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3643   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   3702

Query    998   GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   1057
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3703   GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   3762

Query   1058   ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   1117
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   3763   ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   3822
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Query  1118  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT  1177
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3823  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT  3882

Query  1178  GACGAGTTCTTCTGAG  1193
             ||||||||||||||||
Sbjct  3883  GACGAGTTCTTCTGAG  3898
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>gb|AY952935.1| Expression vector pFNK-101, complete sequence
Length=4099

 Score = 1471 bits (796), Expect = 0.0
 Identities = 796/796 (100%), Gaps = 0/796 (0%)
 Strand=Plus/Minus

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Query  398   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC  457
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4020  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC  3961

Query  458   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA  517
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3960  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA  3901

Query  518   GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG  577
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3900  GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG  3841

Query  578   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG  637
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3840  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG  3781

Query  638   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG  697
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3780  CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG  3721

Query  698   GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG  757
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3720  GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG  3661

Query  758   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC  817
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3660  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC  3601

Query  818   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA  877
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3600  ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA  3541

Query  878   GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC  937
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3540  GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC  3481

Query  938   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT  997
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3480  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT  3421

Query  998   GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC  1057
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3420  GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC  3361

Query  1058  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC  1117
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3360  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC  3301

Query  1118  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT  1177
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3300  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT  3241

Query  1178  GACGAGTTCTTCTGAG  1193
             ||||||||||||||||
Sbjct  3240  GACGAGTTCTTCTGAG  3225
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>gb|AY952936.1| Expression vector pINV-110, complete sequence
Length=4887

 Score = 1471 bits (796), Expect = 0.0
 Identities = 796/796 (100%), Gaps = 0/796 (0%)
 Strand=Plus/Minus

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Query   398   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   457
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   4751  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   4692

Query   458   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   517
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Sbjct   4691  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   4632

Query   518   GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   577
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   4631  GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   4572

Query   578   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   637
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   4571  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   4512

Query   638   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   697
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   4511  CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   4452

Query   698   GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   757
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   4451  GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   4392

Query   758   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   817
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   4391  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   4332

Query   818   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   877
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   4331  ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   4272

Query   878   GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   937
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   4271  GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   4212

Query   938   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   997
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Sbjct   4211  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   4152

Query   998   GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   1057
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   4151  GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   4092

Query   1058  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   1117
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Sbjct   4091  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   4032

Query   1118  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   1177
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   4031  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   3972

Query   1178  GACGAGTTCTTCTGAG      1193
              ||||||||||||||||
Sbjct   3971  GACGAGTTCTTCTGAG      3956
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>gb|DQ225747.1| Gene trapping Ds/T-DNA vector pUR224NB, complete sequence
Length=22828

 Score = 1471 bits (796), Expect = 0.0
 Identities = 796/796 (100%), Gaps = 0/796 (0%)
 Strand=Plus/Plus

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Query   398   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   457
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Sbjct   4659  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   4718

Query   458   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   517
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Sbjct   4719  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   4778

Query   518   GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   577
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   4779  GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   4838

Query   578   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   637
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Sbjct   4839  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   4898
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Query  638   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   697
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Sbjct  4899  CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   4958

Query  698   GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   757
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4959  GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   5018

Query  758   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   817
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Sbjct  5019  CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   5078

Query  818   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   877
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  5079  ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   5138

Query  878   GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   937
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Sbjct  5139  GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGAC   5198

Query  938   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   997
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Sbjct  5199  GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT   5258

Query  998   GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   1057
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Sbjct  5259  GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   5318

Query  1058  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   1117
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  5319  ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   5378

Query  1118  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   1177
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Sbjct  5379  CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   5438

Query  1178  GACGAGTTCTTCTGAG   1193
             ||||||||||||||||
Sbjct  5439  GACGAGTTCTTCTGAG   5454
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>gb|DQ225746.1| 🖾 Gene trapping Ds/T-DNA vector pUR224NA, complete sequence
Length=22828

 Score = 1471 bits (796), Expect = 0.0
 Identities = 796/796 (100%), Gaps = 0/796 (0%)
 Strand=Plus/Minus

```
Query  398   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   457
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  8509  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC   8450

Query  458   GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   517
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Sbjct  8449  GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA   8390

Query  518   GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   577
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  8389  GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG   8330

Query  578   CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   637
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Sbjct  8329  CAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG   8270

Query  638   CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG   697
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Query  698   GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   757
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Sbjct  8209  GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG   8150

Query  758   CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC   817
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Query  818   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   877
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Sbjct   8089   ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA   8030

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Query    938   GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT    997
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Query    998   GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC   1057
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Query   1058   ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   1117
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Sbjct   7849   ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC   7790

Query   1118   CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   1177
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Sbjct   7789   CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTT   7730

Query   1178   GACGAGTTCTTCTGAG   1193
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Sbjct   7729   GACGAGTTCTTCTGAG   7714
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